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25 354 66.2 155 5 AAU90993 AAbb07704 Abb07704 Bowine pe Aau90993 Transplan Adv08371 27 354 66.2 155 5 AAU90998 Abx08371 Aau90993 Transplan Adv08371 29 352.5 65.9 159 5 AAU90998 Abx08376 Adx08371 Adx08371 Bacceneci 29 352.5 65.9 159 5 AAU90998 Adx08376 BAcceneci Bacceneci 30 350 65.4 172 9 AAN2836 Adx08376 BAcceneci Bacceneci		RESULT 1 ADJ82974 ADV82974 ADV82974 AC ADJ82974; AC ADJ82974; AX Mochay-2004 (first entry) AX Moral mucositis; oral lesion; cystic fibrosis; respiratory infection; AX AX ADJ82974; AX	15-JAN-2004. 30-JUN-2003; 2003WO-EP006930. 08-JUL-2002; 2002US-0394486P. 07-JAN-2003; 2003US-0438602P. (GENE-) GENEFROT INC. Bougueleret L, Jeandenans C, Niknejad A; WPI; 2004-099371/10. Novel Pep714-related polypeptide having biological activity, useful for treatment and prevention of microbial or viral infection, cystic fibrosis and chronic respiratory infections. Disclosure; Page 92-93; 99pp; English. The present invention relates to a Pep714-related peptide. This is useful for inhibiting microbial propagation, preferably viral propagation, and in the treatment of chemotherapy and radiotherapy induced oral mucositis, oral lesion, ventilator associated pneumonia, chronic respiratory infections and cystic fibrosis. The present sequence is a Pep714-related peptide precursor protein shown in the exemplification of the invention. Sequence 140 AA; Query Match 100.0%; Score 535; DB 8; Length 140;
GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd. rotein - protein search, using sw model on: January 12, 2006, 21:41:48; Search time 53.6679 Seconds (without alignments) 826.886 Million cell updates/sec e: US-10-815-562-2_COPY_31_131 ence: 1 QVLSYKEAVLRAIDGINQRSVTLNQARGSFDISCDKDNKR 101 ing table: BLOSUM62 Gapop 10.0, Gapext 0.5 ched: 2443163 seqs, 439378781 residues 1 number of hits satisfying chosen parameters: 2443163	0000000 Match	Maximum Match Listing first A Geneseq_21:* Geneseqp198 Geneseqp198 Geneseqp2006 Geneseqp2009 Gen	## SUMMARIES Guery Query Query Query Query Adject Sis 100.0 140 8 ADJ82274 Adj82974 Human Pep Sis 100.0 170 2 AAR92924 Add70379 Human CAP Sis 100.0 170 2 AAR92924 Add70379 Human CAP Sis 100.0 170 5 AAR92924 Add70396 Transplan Sis 100.0 170 6 ADJ2982 Add2987 Add18279 Procein s Adj82973 Human Cat Adj82974 Human Cat Ad

Total number

Searched:

Minimum | Maximum |

Scoring table:

Title: Perfect score:

Sequence:

OM protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not well suited for isolating cDNA primed cDNA libraries such 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                           9
                                                          QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDDPRPTWDGDPDTPKPVSFTVKETVCPRTT 60
                                                                                                                                                                                                                                                                                        expressed sequence tag; secreted protein; cDNA isolation;
                                          QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; SEQ ID NO 7862; 71pp + Sequence Listing; English.
                  Indels
                                                                                                           QOSPEDCDFKCOGLVKRCMGTVTLNQARGSFDISCDKONKR 101
                                                                                             61 QOSPEDCDFKXDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
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100.0%; Pred. No. 1.1e-56;
ive 0; Mismatches 0;
      9.6e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duclert A, Giordano J;
100.0%; Prec. ...
                                                                                                                                                                                                                                                               Human secreted protein, SEQ ID NO: 7862.
                                                                                                                                                                                   AAG03781 standard; protein; 152 AA
                                                                                                                                                                                                                                                                                                      gene therapy; chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                       (first entry)
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Matches 101; Conservative
                  Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
N-PSDB; AAC03787.
     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 152 AA;
                                                                                                                                                                                                                                                                                          Human; 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                              AAG03781;
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The invention relates to a novel polypeptide composition for preventing disease in an organism which comprises one or more types of polypeptide which have an alpha-helix structure and/or thionine component. The composition of the invention demostrates antibacterial and antifugal activities and may be useful for preventing a disease in an organism, for generating cultivated plants and in providing resistance to plant tissue against fungi such as Pyricularia oryzae (rice blast fungus), ceratocystis fimbriate and bacteria euch as Pseudomonas etc. The composition has high antimicrobial activity at low concentration. The current sequence is that of the rabbit CAP18 full-length protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial polypeptide composition for a plant pathogen, comprises one or more types of thionine and/or a polypeptide having an alpha helix structure, as an active ingredient.
                                                                                                                                                                                                                                                                                                                                                                                       alpha-helix; thionine; antibacterial; antifungal; plant;
fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria;
Pseudomonas; antimicrobial; rabbit; CAP18.
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94 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 134
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Pred. No. 1.2e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TOYW ) TOYOTA CHUO KENKYUSHO KK.
                                                                                                                                                                      ADK70797 standard, protein; 169
                                                                                                                                                                                                                                                                                                                                      Human CAP18 full-length protein.
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Best Local Similarity
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                                                                                                                                                                                                                               ADK70797;
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AAR92924
ID AAR;
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                                                                                                                                               ADK70797
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Indels

QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 93

61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101

1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT

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11 QVLSYKEAVLRAIDGINQRSSDANLYRLLDDDPRPTMDGDPDTPKPVSFTVKGTVCPRTT 90
                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a human cationic protein, having lipopolysaccharide binding and anticoagulant activity. The polypeptide designated CAPIB. Amino acids 134-170 of CAPIB represent a reactive nitrogen inhibitory protein (RNIP). The CAPIB polymclectide is useful for producing cationic proteins. The CAPIB polypeptide is useful for treating and disposanting lipopolysaccharide-associated conditions such as gram negative sepsis, and/or coagulation-related disorders, such as disseminated intravascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; cathelicidin; antimicrobial; immunostimulant; immune response; antigen presenting cell; adjuvant; human; antibiotic; FALL-39.
                                                                                                                                                                                                                                                                                       Novel human cDNA encoding cationic proteins having lipopolysaccharide binding and anticoagulant activity, useful for treating and diagnosing gram negative sepsis and disseminated intravascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
/note= "reactive nitrogen inhibitory protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human peptide antibiotic FALL-39 precursor sequence.
                                                                                                                                                                                                                                                                                                                                               Disclosure, Col 29-30; 46pp; English.
                                                                                                                                                                                                                      Hirata M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB07707 standard; peptide; 170
                                                                                                        92US-00916761.
92US-00916765.
93WO-US006731.
94US-00313681.
96US-00691280.
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                                                                                                                                                                                           (PANO-) PANORAMA RES INC.
                                                                                                                                                                                                                     Larrick JW, Wright SC,
                                                                                                                                                                                                                                                WPI; 2000-531989/48.
                                                                                                                                                                                                                                                             N-PSDB; AAA59574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 170 AA;
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                           US6103888-A.
                                                                                01-JUN-1099;
                                                      15-AUG-2000.
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27-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cationic protein; lipopolysaccharide binding; anticoagulant; CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis; coagulation-related disorder; disseminated intravascular coagulation.
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                            FALL-39; cathelin; antibiotic; antimicrobial; antibacterial.
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                                                                                              1. .131
/label= Prepro-peptide
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                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                          resistance and is non-cytotoxic.
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                                                                                                                        132. .170
/label= FALL-39
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                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT18233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 170 AA;
Prepro-FALL-99
                                                       Homo sapiens
                                                                                                                                                                 WO9608508-A1
                                                                                                                                                                                                                                                13-SEP-1994;
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preservation of organs prior to transplant.
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Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vulnerary; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BALS/) BALS R.
(KOCZ/) KOCZULLA A R.
(VDEG/) VON DEGENFELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bals R, Koczulla AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-879818/82.
N-PSDB; ADF18220.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 170 AA;
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#X & X O O O O O O O O O O O O O O O X &
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                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a vaccine comprising at least one antigen and at least one catholicidin derived antimicrobial peptide or its derivative. The vaccine is useful for active immunization, especially of humans or animals without protection against the specific antigen. The catholicidin derived antimicrobial peptide is useful in the preparation of an adjuvant for enhancing the immune response to at least one antigen, where the adjuvant enhances the uptake of at least one antigen, where the presenting cells (APC), and the adjuvant is added to the vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                 Vaccine for active immunization or for preparing an adjuvant for enhancing an immune response to at least one antigen, comprises at least one antigen and at least one cathelicidin derived antimicrobial peptide.
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                                                                                        Egyed A;
                                                                                        Buschle M,
                           (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU90996 standard; peptide; 170 AA
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                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1, 65pp, English.
                                                                                     Zauner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-JUL-2001; 2001WO-US023785.
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17-NOV-2000; 2000US-0249602P.
15-MAY-2001; 2001US-0290932P.
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                                                                                     Mattner F,
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                                                                                                                                                WPI; 2002-269154/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 170 AA;
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                                                                                     Pritz J,
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The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface creeptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant, animals receiving kidneys stored in the creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys alone. Lower serum creatinine levels are indicative of healthier kidneys alone. Lower serum creatinine levels are indicative of healthier kidneys come and a more preferable prognosis for the transplant patient. The media of the incidence and/or severity of delayed graft function in patients receiving transplant of healthier corgans leads to a decrease in chronic rejection. This sequence represents an antimicrobial peptide studied in the development of the transplant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 170;
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100.0%; Pred. No. 1.2e-56;
ive 0; Mismatches 0;
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Disclosure; Page 27; 78pp; English
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The present invention is based on the finding that human antimicrobial peptide LL-37 ADF18218 is capable of inducing functionally important angles in cell culture and in vivo by activation of the receptor molecule FPRAL1. LL-37 can be used in the preparation of a pharmaceutical composition for the prevention or treatment of a disease caused by, or cresulting in, a reduced level of angiogenesis or arteriogenesis, or for the treatment of (infected) wounds or cancer. The disease may be associated with reduced blood flow, such as atherosclerosis, coronary heart disease, stroke, arterial occlusive disease or an ulcer. Suppression of angiogenesis through inhibition of IL-37 can be used to treat tumours, especially a carcinoma or sarcoma including cancer of the bile duct, brain, breast, colon, stomach, male and female reproductive cryans, lung and altraways, skin, gallaladder, liver, nasopharynx, nerve cells, kidney, prostate, and Kaposi's sarcoma (all claimed). The present protein sequence is not explained in the specification.
Use of a peptide LL-37 for the preparation of a composition for preventing or treating wounds or a disease caused reduced blood flow, e.g. atherosclerosis, coronary heart disease, stroke, arterial occlusive
                                                                                                                                                Disclosure, Page, 15pp, English.
                                                                                           diseases or ulcer.
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Sequence 170 AA;

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                                                                        QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                              Gaps
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Length 170;
                           0; Indels
                                                                                                               61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
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100.0%; Score 535; DB 7;
100.0%; Pred. No. 1.2e-56;
iive 0; Mismatches 0;
 Query Match 100.
Best Local Similarity 100.
Matches 101; Conservative
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ADP65263 standard; protein; 170 AA 12-AUG-2004 ADP65263;

Human cathelicidin antimicrobial peptide. 🗸 (first entry)

rheumatoid arthritis; collagen-induced; Immunosuppressive; antirheumatic; antiathritis; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis; autoimmune disease; arthritide; gene expression analysis; immune; human

Homo sapiens

WO2003072827-A1 04-SEP-2003.v 31-OCT-2002; 2002WO-US035433.

31-OCT-2001; 2001US-0336220P

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

Thorton SL Hirsch R,

WPI; 2003-712740/67. GENBANK; NP_004336. Diagnosing and analyzing autoimmune disease using gene expression

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The regults in a give expression signature of the mark, and using that gene expression signature to diagnature to the manalyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention of turther comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal of the array or gene chip, specific for rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; diagnosis or analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagentinduced arthritis; and reducing the symptoms associated with collagentinduced arthritis; and reducing the symptoms associated with collagentinduced arthritis; and reducing the symptoms associated with collagentinduced arthritis; and reducing of the invention have the following artifications of the present invention are useful for methods and compositions of the present invention are useful for theumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, and an immune disease caused by an infectious agent. This sequence repartement of immune disease or arthritides. Note shown in the specification. It has been supplied in an electronic format from
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profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                    The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that
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                                                                                                     Disclosure; Page; 56pp; English
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CAP18; cationic antimicrobial protein of 18 kDa; bacterial pneumonia; chronic lung disease; acute lung disease; inflammatory lung disease; ARDS; bronchial asthma; human. ADI29582 standard; protein; 170 AA. 22-APR-2004 (first entry) Human CAP18, SEQ ID ADI29582; RESULT 10 ADI29582 셤

WO2004009640-A1. 29-JAN-2004

Homo sapiens.

22-JUL-2003; 2003WO-JP009267.

22-JJL-2002; 2002JP-00213040. 14-MAR-2003; 2003JP-00070932.

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WO2004005338-A1
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Matches
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                                                                                                             The present invention relates to a novel CAP18 (cationic antimicrobial protein of 18 kDa) antibody that can bind with human CAP18 peptide fragments AD129579-AD129581. The antibody is useful in reagents and kits for the detection, diagnosis and monitoring bacterial pneumonia and other CAP18-related diseases like chronic and acute lung diseases, inflammatory
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                                                       New antibody against an antibacterial peptide, particularly human CAP18, applicable in reagents and kits for detection, diagnosis and monitoring of bacterial pneumonia.
                                                                                                                                                              diseases, ARDS and bronchial asthma. The present sequence is human
                                                                                                                                                                                                                                                            QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTWDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 pep714-related peptide; precursor; human; secreted peptide; Pep714; oral mucositis; oral lesion; cystic fibrosis; respiratory infection;
                  Hashimoto
                                                                                                                                                                                                                               ö
                                                                                                                                                                                                             Length 170
                  Ishizaka A,
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "dibasic peptidase cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "dibasic peptidase cleavage site"
                                                                                                                                                                                                                                                                                      QQSPEDCDFKKDGLVKRCMGTVTLNQARGSPDISCDKDNKR 101
                                                                                                                                                                                                                                                                                                  OOSPEDCDFKKOGLVKRCMGTVTLNOARGSFDISCDKDNKR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= antibacterial_protein_FALL-39
134. .170
/label= antibacterial_protein_LL-37
                                                                                                                                                                                                                                                                                                                                                                                                               Human Pep714-related peptide precursor SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "dibasic peptidase cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "dibasic peptidase cleavage
151. .152
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                                                                                                                                                                                                           Query Match
100.0%; Score 535; DB 8;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 101; Conservative 0; Mismatches 0;
                  Tamura H,
                                                                                             Disclosure; SEQ ID NO 4; 52pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l. .30
/label= Bignal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       ADJ82973 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= propeptide
106. .107
                  Naiki Y,
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140. .141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .131
                  Toyooka K,
(SEGK ) SEIKAGAKU CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note
                                     WPI; 2004-143269/14
                                                                                                                                                                                          Sequence 170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cleavage-site
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                  Kirikae T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumonia
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                                                                                                                                                                                                                                                                                                                                                             Novel Pep714-related polypeptide having biological activity, useful for treatment and prevention of microbial or viral infection, cystic fibrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          infection; cathelicidin type peptide; LL-37; antimicrobial;
antiinflammatory; immunostimulant; bacterial infection; neutropenia;
toothpaste; mouthwash; gingivitis; oral infection; periodontitis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDBFRPTMDGDPDTFKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                  Niknejad A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 91-92; 99pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      and chronic respiratory infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Puetsep K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN41827 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human LL-37 protein SEQ ID NO:2.
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                                                      30-JUN-2003; 2003WO-EP006930
                                                                                                          08-JUL-2002; 2002US-0394486P
07-JAN-2003; 2003US-0438602P
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                                                                                                                                                                                                                                                     Jeandenans
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                                                                                                                                                                                              (GENE-) GENEPROT INC
                                                                                                                                                                                                                                                                                                         WPI; 2004-099371/10.
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N-PSDB; ADN41826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 170 AA;
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15-JAN-2004
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The present invention describes a method for determining the susceptibility of a subject to infection. The method comprises: (i) providing a sample from a subject; (ii) detecting any cathelicidin type providing a sample from a subject; (iii) detecting any cathelicidin type comprises that subject to infection (where no LL-37) and a control sample; (iv) determining the susceptibility of the subject to infection (where no LL-37) and (v) level of LL-37 indicates that subject is susceptible to infection; and (v) optionally administering an antimicrobial agent to reduce infection. Also conticosteroid or growth factor (preferably recombinant granulocyte corticosteroid or growth factor (G-CSF) or GM-CSF). The product has attimicrobial, antimifalmamatory and immunostimulant activities. The method can be used for determining the susceptibility of a subject to infection such as bacterial infection (e.g. Actinobacillus cationovycetemcomitans infection) and neutropenia, and for diagnosing neutropenia (e.g. Kostmann morbus). The method is also useful in the manufacture of a medicament in the form of toothpaste or mouthwash for the preventative treatment of infection e.g. spingivitis, oral infection (such as periodonitis), and for the treatment of neutropenia. The method controls the normal flora in neutropenia and so combat infections. The present sequence represents the proform of human LL-37, which is used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Evaluating cystic pulmonary fibrosis, by measuring cationic antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
            Determination of susceptibility of subject to infection comprising detecting cathelicidin type peptide present in sample, optionally comparing level of peptide in sample to control sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cystic pulmonary fibrosis; cationic antimicrobial protein; CAP18; pulmonary disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 QQSPEDCDFKKOGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 535; DB 8;
100.0%; Pred. No. 1.2e-56;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cationic antimicrobial protein-18.
                                                                                                 Disclosure; SEQ ID NO 2; 40pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 170 AA;
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The invention relates to a novel method for evaluating cystic pulmonary fibrosis. The method comprises: measuring the quantity of cationic attimicrobial protein of 18 KDR (CAR18) in the biological sample collected from the individual; comparing the quantity of CAR18 measured in the previous step and the quantity of CAR18 in a control sample; and evaluating cystic pulmonary fibrosis by associating comparison of obtained results. The invention further comprises: a kit for carrying out the evaluating method, comprising a solid-phase component and an antibody coupled with an antigenic peptide having a sequence of ADR47312, or a solid-phase component comprising an solid-phase omponent comprising an immobilised antibody (first antibody) which is coupled with the antigenic peptide. The method or kit are attibody) coupled with the antigenic peptide. The method or kit are useful for evaluation of solid-phase solid-phase diagnosis for the presence or absence of a risk of cystic pulmonary fibrosis, evaluation of serious or acute conditions, or the evaluation of the advanced grade of the disease. The method accurate evaluation of the acute or serious conditions, or the evaluation of the pulmonary diseases. This sequence represents the human conditions.

CAP18 protein of the pulmonary diseases. This sequence represents the human conditions.
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protein of 18 kDa (CAP18) quantity in biological sample, and evaluating fibrosis by comparing measured quantity and quantity of CAP18 in control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSPTVKBTVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 535; DB 8;
Pred. No. 1.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                 Disclosure; SEQ ID NO 4; 14pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-2002; 2002US-0414971P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 170 AA;
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                                            ващрје.
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(EURO-) EUROSCREEN SA.

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The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide perves as least 80% identical to the TAT nucleic acids and polypeptide polypeptides; expression vectors and host cells compitating a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or aliagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, inver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central cancer, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide.
                                                                                                             New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                         Claim 12; SEQ ID NO 1129; 7273pp; English.
                                                                                                                                                                                                      prostate cancer or tumor.
                             WPI; 2004-347921/32.
                                                     N-PSDB; ACN37923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 170 AA;
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                                                                               9
                                                                                                                    90
                                                                               1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                  31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                       0; Gaps
100.0%; Score 535; DB 8; Length 170; 100.0%; Pred. No. 1.2e-56; ive 0; Mismatches 0; Indels (
                                                                                                                                                              61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
                                                                                                                                                                                 91 QOSPEDCDFKGGGLVKRCMGTVTLNQARGSFDISCDKDNKR 131
                                   Matches 101; Conservative
  Query Match
Best Local Similarity
                                                                               8
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Mouse chemerin peptide SEQ ID NO 51.
                                                                                                                                          ADW43827 standard; peptide; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-2005
                                                                                                                                                                                                                                                                                     ADW43827;
RESULT 15
ADW43827
ID ADW43
XX
AC ADW43
XX
DT 24-MA
XX
XX
MW Gene
XW G
```

gene therapy; diagnosis; cell signaling; gene therapy; lymphoproliferative disease; dermatological disease; dermatological; demostatic; inflammation; antiinflammartory; hematological disease; immune disorder; neoplasm; cardiovascular-gen.; cns-gen.; neoplasm; cardiovascular-gen.; cns-gen.; neoplasm; cardiovascular-gen.; cns-gen.; chemerin.

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whe musculus
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WO2005000875-A2

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25-JUN-2004; 2004WO-EP006945.
                                                       25-JUN-2003; 2003US-00603566
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The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a chemering polypeptide. Also comprising the coding sequence of the nucleic acid; a transgenic animal transferred with the expression vector; a (therapeutic) composition or comprising (I) and an isolated Chemering Polypeptide or a nucleic acid agreement of the modulates the interaction between a Chemering polypeptide or an aucheic and a gent that modulates the interaction between a Chemering polypeptide on a gent that modulates the interaction between a Chemering polypeptide in a sample; identifying an agent that modulates the interaction between a Chemering polypeptide on a gent that modulates the interaction between a Chemering polypeptide in a sample; of an agent that modulates the interaction between a Chemering Polypeptide on a gent that modulates the function of Chemering Polypeptide; detecting the presence, in a sample, of an agent that modulates the function of Chemering Alsaesae or disorder characterized by dysregulation of Chemering Rpolypeptide is signaling; a kit, for screening agents that modulates the signaling activity of Chemering Polypeptide on a condition of Chemering Polypeptide is signaling; a kit, for a creening adease or disorder characterized by dysregulation of Chemering Polypeptide is signaling, an in ollated polymolectide encoding (I), an isolated polymolectide encoding (I), and it packaging creamed with a polymucleotide encoding (I), and its packaging creamedian in vitro menchod of inhibiting call proliferation. The chemering a disease, e.g. neoplasms, hypergammaglobulinemia, purpura, sarcoldosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, gaucher's bisease, histocytosis, and any other of methods are useful for algenosing and prepared in with perpublication of immature chemering peptides and polymoliferative disease. The polypeptides and polymoliferative disease. The polypeptides and polymoliferative disease. The polypeptides and polymoliferative disease. The polypeptid
                                                                                                                                                                         New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, Gaucher's
                                                Loison C;
                                                Parmentier M,
                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 51; 183pp; English.
                                                Detheux M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      processing of immature chemerin.
                                                                                                                                                                                                                                                         Disease, or histiocytosis.
                                                Wittamer V, Communi D,
                                                                                                                           WPI; 2005-058121/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 170 AA;
                                                                           Ooms FDR;
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Gapa ; 0 100.0%; Score 535; DB 9; Length 170; 100.0%; Pred. No. 1.2e-56; IndelB Mismatches ö Best Local Similarity 100. Matches 101; Conservative Query Match

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Search completed: January 12, 2006, 21:48:09 Job time : 53.6679 secs

Н

OM protein - protein search, using sw model

January 12, 2006, 21:43:14 ; Search time 8.94465 Seconds (without alignments) 1086.448 Million cell updates/sec Run on:

US-10-815-562-2_COPY_31_131 Title: Perfect score:

1 QVLSYKEAVLRAIDGINQRS.....VTLNQARGSFDISCDKDNKR 101 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries 1: pirl: * 2: pirl: * 3: pirl: * 4: pirl: * PIR 80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	CAP18 precursor -	antibacterial pept		antibacterial pept	Ψ	antimicrobial prot	ĭ	~	e	Н	4	protegrin 5 precur	prophenin (PF-2) p	antibacterial prot	18K lipopolysaccha	cathelin-related p	antibacterial pept	bactenecin 5 precu	cathelin-related p	myeloid antimicrob	cathelin-related p	indolicidin precur	cathelin - pig	antimicrobial pept	polymorphonuclear	polymorphonuclear	secreted phosphopr	kininogen, LMW II	kininogen, HMW II
SUMMARIES	g:	138932	S74248	S68229	A53421	S27018	S68232	857330	0060NC	A53895	S57607	B53895	857609	S40463	S41731	JQ1171	S68411	868967	A45328	S68412	S68228	870521	JC1222	XKPGC	868230	B46634	A46634	146051	KGBOL2	KGBOH2
	DB	7	~	~	7	~	7	~	~	~	0	N	N	~	N	7	~	N	~	N	~	~	н	-	7	~	N	~	-	Н
	Length	170	170	155	153	155	172	212	147	149	149	149	149	228	166	171	152	167	176	160	160	173	144	96	190	135	137	200	434	619
d	Query Match	100.0	99.1	68.4	67.5	66.2	65.4	65.4		64.9	64.9	64.9	64.9	64.7	64.3	64.1	63.6	63.6	63.6	62.3	62.3	61.1	60.4	59.6	58.3	27.3	26.9	16.0	15.9	15.9
	Score	535	530	366	361	354	350	350	347	347	347	347	347	346	344	343	340.5	340	340	333.5	333.5	327	323	319	312	146	144		82	82
	Result No.	-	7	e	4	S	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

kininogen, LMW I p	- 5	probable cysteine	spp-24 precursor -	photosystem II oxy	conserved hypothet	photosystem II oxy	photosystem II oxy	kininogen, LMW pre	kininogen, HMW pre	photosystem II oxy	major surface glyc	fragile X mental r	hypothetical prote	photosystem II oxy
KGBOL1	C84397	T05390	G01654	816586	G82903	S04132	T02066	KGHUL1	KGHUH1	T08403	JC2217	S60173	G87536	S11852
- -	1 (7	0	7	~	~	N	N	-	7	~	~	N	~	7
436	263	355	211	332	364	329	332	427	644	331	1076	673	312	332
15.7	14.8	13.6	13.6	13.6	13.4	13.0	13.0	12.9	12.9	12.8	12.8	12.7	12.4	12.4
48	79	73	72.5	72.5	71.5	69.5	69.5	69	69	68.5	68.5	68	66.5	66.5
30	125	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 138932
R;Larrick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.
R;Larrick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.
A;Title: Human CAPI8: a novel antimicrobial lipopolysaccharide-binding protein.
A;Reference number: 138932; MUID:95197251; PMID:7890387 CAP18 precursor - human

A;Accession: 138932 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-170 <RES>

A;Cross-references: UNIPROT:P49913; UNIPARC:UPI000000A67; EMBL:U19970; NID:g643476; PID C;Superfamily: cathelin; cystatin homology C;Superfamily: cystatin homology <CYS>

Gapa ö Length 170; 0, Indels 100.0%; Score 535; DB 2; 100.0%; Pred: No. 1.9e-50; tive 0; Mismatches 0; Query Match Best Local Similarity 100.0 Matches 101; Conservative

ö 9 90

31 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT н 셤 ઠે

QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101 ò 셤

RESULT 2

NyAlternate names: antibacterial peptide PALL39
NyAlternate names: antibacterial peptide PALL39
NyContains: antibacterial peptide LL-37; cathelin-related antibacterial peptide CAP-18
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence revision 06-Feb-1998 #text change 09-Jul-2004
C;Accession: S74248; S78211; \$66281; S66205; A55596; S49441; S58023
Eur. J. Biochem. 238, 325-332, 1996
A;Title: The human gene FALL39 and processing of the cathelin precursor to the antibacte A;Reference number: S74248; MUID:96283824; PMID:8681941

A; Accession: S74248

A; Molecule type: DNA A; Residues: 1-170 <GUD>

A; Cross-references: UNIPROT: P49913; UNIPARC: UP1000017636C; EMBL: X96735

A, Accession: S78211

A;Molecule type: protein A;Residues: 134-143 «GUR» TCROSS-TEFERENCES: UNIDARC:UP1000017636D R;Cowland, J.B.; Johnsen, A.H.; Borregaard, N.

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antibacterial peptide precursor - pig
Cispecies: Sus scroca domestica (domestic pig)
Cipate: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
Cipate: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
Cipatesion: A53421
R;Zanetti, M.; Storici, P.; Tossi, A.; Scocchi, M.; Gennaro, R.
R;Zanetti, M.; Storici, P.; Tossi, A.; Scocchi, M.; Gennaro, R.
A;Title: Molecular cloning and chemical synthesis of a novel antibacterial peptide deriv
A;Reference number: A53421; MUID:94179144; PMID:8132502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Romeo, D.; Skerlavaj, B.; Bolognesi, M.; Gennaro, R.
J. Biol. Chem. 263, 9573-9575, 1988
A;Title: Structure and bactericidal activity of an antibiotic dodecapeptide purified fro.
A;Reference number: A33799; MUID:88257074; PMID:3290210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P49930; UNIPARC:UPI000012F425; GB:L26053; NID:9468911; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-155 <STO>
A;Cross-references: UNIPROT:P22226; UNIPARC:UPI0000049485; GB:L08834; NID:g162599; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: cDNA sequence analysis of an antibiotic dodecapeptide from neutrophils A;Reference number: S27018; MUID:93093170; PMID:1459251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bactenecin precursor - bovine
NiAlternate names antiblotic dodecapeptide
CiSpecies: Bos primigenius taurus (cattle)
CiSpacies: Bos primigenius taurus (cattle)
CiSpaces 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
CiAccession: S27018; A33799
FRS:Storici, P.; del Sal, G.; Schneider, C.; Zanetti, M.
FEBS Lett. 314, 187-190, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 QALSYREAVLRAVDRLNEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCPRPT
30 QVLSYREAVLRAVDQLNEQSSEPNIYRLLELDQPPQDDEDPDSPKRVSFRVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fil. 29/Domain: signal sequence #status predicted <SIG>
Fi22-129/Domain: cystatin homology <CYS>
Fi30-143/Domain: propeptide #status predicted <PRO>
Fi144-155/Product: bactenecin #status experimental <MA1
Fi146-154/Disulfide bonds: #status experimental
                                                                                           61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bolognesi, M.; Gennaro, R. 75, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 68.0%; Pred. No. 1.1e-31;
Matches 66; Conservative 17; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: cathelin; cystatin homology C;Keywords: antibacterial P;22-129/Domain: cystatin homology <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Experimental source: neutrophils
C,Superfamily: cathelin; cystatin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 144-155 <ROM>
A;Cross-references: UNIPARC:UP1000003532B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Keywords: antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-153 < ZAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A53421
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S27018
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                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Molecule type: protein
A; Residues: 42-49;50-57; 78-65, 7X', 67-85, 7X', 87-96, 7X', 98-100;110-112, 7T', 114-152 < COF>
A; Residues: 42-49;50-57; 78-65, 7X', 67-85, 7X', 87-96, 7X', 98-100;110-112, 7T', 114-152 < COF>
A; Cross-references: UNIPARC: UPI000017636F; UNIFARC: UPI0000176370;
B; Agerberth, B.; Gunne, H.; Odeberg, J.; Kogner, P.; Boman, H.G.; Gudmundsson, G.H.
Proc. Natl. Acad. Sci. U.S.A. 92, 195-199, 1995
A; Title: FMLL-39, a putative human peptide antibiotic, is cysteine-free and expressed in A; Reference number: A55596; MUID:95116523; PMID:7529412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Map position: 3
A.Introns: 67/3; 103/3; 127/3
A.Introns: 67/3; 103/3; 127/3
A.Introns: 67/3; 103/3; 127/3
A.Introns: 67/3; 103/3; 127/3
C.Superfamily: cathelin; cystatin homology
C.S.E.May.Mar. antibacterial; blocked amino end; pyroglutamic acid
F;1-30/Domain: signal sequence #status predicted <SIM>
F;22-130/Domain: cystatin homology <CYS>
F;31-130/Product: cathelin-related antibacterial peptide CAP-18 #status predicted <MATI>F;31-133/Domain: propeptide #status predicted <PRO>
F;31-133/Domain: propeptide #status predicted <ARO>
F;31-134-170/Product: antibacterial peptide LL-37 #status experimental <MAT>
F;31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
                             A;Title: hCAP-18, a cathelin/pro-bactenecin-like protein of human neutrophil specific gr
A;Reference number: S66205; MUID:95339969; PMID:7615076
A;Accession: S66281
                                                                                                                                                                                   A;Molecule type; mRNA
A;Residues: 1-117,'T',114-170 <COW>
A;Cross-references: UNIPARC:UP10000000A67; EMBL:X89658; NID:g902627; PIDN:CAA61805.1; PI
A;Accession: S66205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
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A;Reference number: S68228; MUID:96105386; PMID:7498547
A;Reference number: S68228; MUID:96105386; PMID:7498547
A;Accession: S68229
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 - CARGA
A;Residues: 1-155 - CARGA
A;Cross-references: UNIPROT:F54230; UNIPARC:UPI0000126859; EMBL:L46853; NID:g1161246; E
C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>F;2-129/Domain: cystatin homology control of the sequence for the sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;MOLECULE type: mRNA
A;Residues: 1-5,'N',7-112,'T',114-170 <AGE>
A;Cross-references: UNIPARC:UPI0000000841; EMBL:Z38026; NID:9558378; PIDN:CAA86115.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antimicrobial peptide precursor - sheep
NiAlternate names: procyclic dodecapeptide homolog
CiSpecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
CiSpecies: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
CiAccession: S68229
FR:Bagella, L.; Scocchi, M.; Zanetti, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.1%; Score 530; DB 2; 99.0%; Pred. No. 6.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.4%; Score 366; DB 2;
69.8%; Pred. No. 3.2e-32;
tive 16; Mismatches 13;
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    Lett. 368, 173-176, 1995
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Best Local Similarity
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Best Local Similarity
Matches 67; Conserva
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a ઠે 셤 66.2%; Score 354; DB 2; Length 155;

Query Match

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cathelin-like antibacterial peptide precursor (clone C6) - pig (fragment)
NyAlternate names: antimicrobial peptide; prophenin-1
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57330; S68726
R;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V
Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte
A;Reference number: S57330; MUID:96042752; PMID:7576250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Realdues: 1-212 <STR>
A; Realdues: 1-212 <STR>
A; Cross-rences: 1-212 <STR>
A; Cross-rences: UNIPROT: PS1524; UNIPARC: UPI0000131712; GB: X86031; NID: g1006756; PIDN
B; Harwig, S.S.L.; Kokryakov, V.N.; Swiderek, K.M.; Aleshina, G.M.; Zhao, C.; Lehrer, R.I
FEBS Lett. 362, 65-69, 1995
A; Title: Prophenin-1, an exceptionally proline-rich antimicrobial peptide from porcine 1
A; Reference number: $68726; MUID: 95212585; PMID: 7698355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-147 <STO>
A;Cross-references: UNIPROT:P32195; UNIPARC:UPI0000131776; GB:L24745; NID:g431435; PIDN:
R;Mirgordskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: protein
A,Residues: 131-146 <MIR>
A,Crose-references: UNPARC:UP1000014310F
R,Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M., Sh
PEBS Lett. 327, 231-236, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protegrin 2 precursor - pig
NiAlternate names: cathelin-like protein precursor; neutrophil peptide 3
Cispeciae: Sus scrofa domestica (domestic pig)
Cipate: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
CiAccession: JN0900; S36822; S34586
Ristorici, P.; Zanetti, M.
Biochem. Biophys. Res Commun. 196, 1363-1368, 1993
A;Title: A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide with a A;Reference number: JN0900; MUID:94071898; PMID:8250892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 QALSYREAVLRAVDRLMEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCPRPT
30 QALSYREAVLRAVDRIMEQSSEANLYRLILEIDQPPKADEDPGTPKPVSFTVKETVCPRPT
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ilarity 64.4%; Pred. No. 2.4e-30;
Conservative 18; Mismatches 18.
                                                                                      61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK
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C, Superfamily: cathelin; cystatin homology
C, Keywords: antibacterial
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A;Residues: 131-209 <HAR>
A;Cross-references: UNIPARC:UP1000014595E
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ses 65; Conserv
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Best Local S
Matches 65
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A;Molecule type: DNA
A;Residues: 1-172 <2HA>
A;Cross-references: UNIPROT:P80054; UNIPARC:UPI000013215A; EMBL:X89201; NID:g1165150; PI
A;Experimental source: laukocytes
R;Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A;Reference number: JN0899; MUID:94071853; PMID:8250863
A;Hitle: A CDNA derived from pig bone marrow cells
A;Reference number: JN0899; MUID:94071853; PMID:8250863
A;Holecule type: mRNA
A;Residues: 1-20, 'A,'22-172 <STO>
A;Rolecule type: mRNA
A;Residues: 1-20, 'A,'22-172 <STO>
A;Rolecule type: mRNA
A;Residues: 1-20, 'A,'22-172 <STO>
A;Rolecule type: mRNA
A;Residues: 1-20, 'A,'30-89, '085-7089, 1995
A;Ritle: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam
A;Reference number: 147138; MUID:95350216; PMID:764374
A;Accession: 147138
A;Accession: 147138
A;Accession: 147138
A;Accession: 147138
A;Accession: MAID:95350216; PMID:7624374
A;Accession: 147138
A;Residues: reliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: reliminary; translated from GB/EMBL/DDBJ
A;Accession: 147138
A;Accession: UNIPARC:UPI00016CGAC; EMBL:X87236; NID:g829142; PIDN:CAA60682.1; PI
R;Agerberth, B; Lee, J:*, Bergman, T:; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall
R;Agerberth, B; Lee, J:*, Bergman, T:; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall
Bur. J. Biochem. 202, 849-854, 1991.
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C;Keywords: amidated carboxyl end, antibacterial
C;Keywords: amidated carboxyl end, antibacterial
C;Keywords: amidated carboxyl end, antibacterial
F;12-139/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>
F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen A;Reference number: S68232; MUID:96105365; PMID:7498226
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                                                                                                                                                                QALSYREAVLRAVDQLNEQSSEPNIYRLLELDQPPQDDEDPDSPRRVSFRVKETVCSRTT 89
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antimidrobial protein PR-39 precursor, cathelin-associated - pig
N.Alternate names: myeloid antibacterial protein PR-39
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68232; July 138; S19563
R;Zhao, C.; Ganz. T.; Lehrer, R.I.
PRBS Lett. 376, 130-134, 1995
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       67.7%; Pred. No. 6.4e-31; indels ive 16; Mismatches 15; Indels
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A,Residues: 13.1-169 <AGRS.
A;Cross-references: UNIPARC:UPI00002D613
A;Experimental source: intestine
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                                                  65; Conservative
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Best Local Similarity
Matches 66; Conserva
       Similarity
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       Best Local
Matches 6
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F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 3 #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
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A; ARCERENGENCE NUMBER: S05285; MUID: 993594835; FMLU: 702804
A; ARCERIOUN: 566285
A; MCGCOLDE 1-149 <-ZH3>
A; RESIDAO, C; 1, Lidu, L; Lehrer; R.I.
FEBS. Cett. 346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: 845712; MUID: 94283613; PMID: 8013647
A; Atcession: A346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Accession: A3485
A; Atcession: A3485
A; Atcession: A3485
A; Arcession: A3485
A; MOID COULD COMPARE WITH CONCEPTURING A; SHOWN CONTROL COMPARE WITH A; MOID COULD 
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost A,Reference number: S34585; MUD:9337946; PMID:833513
A;Accession: S34586
A;Accession: S34586
A;Accession: S34586
A;Residues: 131-146 < KOK.
A;Cross-references: UNIPARC:UPI000014310F
C;Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>F;2-129/Domain: cystatin homology <CYS-F;2-129/Domain: cystatin homology <CYS-F;3-146/Product: protegrin 2 #status experimental <NAT>F;146/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl
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NyAlternate names: neutrophil peptide 2
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1995 #sequence revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S66285; A53895; S34871; S36821; S57608
R;Zhao, C; Ganz, T.; Lehrer, R.I.
R;Zhao, C; Ganz, T.; Lehrer, R.I.
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
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C;Superfamily: cathelin; cyfetatin homology
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: aignal sequence #status predicted <8IG>
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Best Local Similarity
Matches 64; Conserva
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A,Residues: 1-149 <ZHA>
A,Residues: 1-149 <ZHA>
A,Cross-references: UNIPROT: P32194; UNIPARC: UPI0000131775; EMBL: X84094; NID: 9887642; PID: R5Zhao, C.; Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A,Reference number: S45712; MUID: 94283613; PMID: 8013647
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R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
REBS Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: S36820; MUID:93387466; PMID:8375505
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A;Residues: 131-148 <MIR>
A;Residues: 131-148 <MIR>
A;Residues: 131-148 <MIR>
A;Cossareferences: UNIPARC:UPI0000034C2E
B;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; Sh. PEBS Lett. 327, 231-236, 1993
A;Title: Protegatins: leukocyte antimicrobial peptides that combine features of corticost A;Reference number: S34585; WUID:93327946; PMID:8335113
A;Accession: S34585
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Ajintrons: 66/3; 102/3; 126/3
C; Superfamily: cathelin; cystetin homology
C; Keywords: amidated cathoxyl end; antibacterial; neutrophil
F; L29/Domain: signal sequence #status predicted <SIG>
F; 22-129/Domain: cystatin homology <CYS>
F; 21-129/Domain: propeptide #status predicted <PRO>
F; 11148/Product: protegrin 1 #status experimental <MAT>
F; 1148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl);
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NyAlternate names: neutrophila (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Socash; S45712; S36820; S34585; S57607
C;Accession: S66284; S45712; S36820; S34585; S57607
FEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID: 95554835; PMID: 7628604
A;Reference number: S66284
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       DB 2; Length 149;
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Query Match

64.9%; Score 347; DB 2; Length 14

Best Local Similarity 66.0%; Pred. No. 3.5e-30;

Matches 64; Conservative 17; Mismatches 16; Indels
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64.9%; Score 347; DB 2;
Best Local Similarity 66.0%; Pred. No. 3.5e-30;
Matches 64; Conservative 17; Mismatches 16;
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Residues: 131-148 <KOK>
;Cross-references: UNIPARC:UP10000034C2B
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A; Residues: 1-149 <ZH2>
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A;Cross-references: UNIPROT:P51525; UNIPARC:UPI0000131713; EMBL:X75438; NID:g443812; PID R;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V Biol. Chem. Hoppe-Seyler 376, 507-510, 1995
A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte A;Reference number: S57330; MUID:96042752; PMID:7576250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UP10000131713
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
SEBS Lett. 376, 130-134, 1995
A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen
A;Reference number: S68232; MUID:96105365; PMID:7498526
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                                                                                                                                                                                                                                                                                                                                                                                    prophenin (PF-2) precursor - pig
NyAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor NyAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor C; Species Sus scrofa domestica (domestic pig)
C; Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C; Accession: 840463; S57331; $68233
K; Pungercar, U; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, F.; Turk, FEBS Lett. 336, 284-288, 1993
A; Title: Molecular cloning of a putative homolog of proline/arginine-rich antibacterial A; Reference number: $40463; MUID:94085623; PMID:8262247
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                                                                   30 QALSYREAVLRAVDRIANEQSSEANLYRILELDQPPKADEDPGTPKPVSFTVKETVCPRPT 89
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
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                                    QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKRTVCPRTT
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R;Storici, P.; Scocchi, M.; Tossi, A.; Gennaro, R.; Zanetti,
PEBS Lett. 337, 303-307, 1994
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P:1-29/Domain: simal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-228/Product: prophenin (PF-2) #status predicted <MAT>
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Best Local Similarity
Matches 64; Conserv
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A;Molecule type: mRNA
A;Residues: 1-228 <STR>
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A;Molecule type: mRNA
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protegrin 4 precursor - pig
protegrin 4 precursor - pig
C;Bpecies: Sus scrofa domestica (domestic pig)
C;Date: 0.1 bec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Date: 0.1 bec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Date: 0.1 bec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: B53895
R;Zhao, C; 114, L; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A;Title: Identification of a new member of the protegrin family by cDNA cloning.
A;Reference number: S45712; MUID:94283613; PMID:8013647
A;Reture: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-149 cZHA>
A;Gross-references: UNIPROT:P49933; UNIPRAC:UPI0000131778; GB:X83268; NID:g603039; PIDN:C;Superfamily: cathelin; cystatin homology
C;Reywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #statuus predicted <NIG>F;22-129/Domain: cystatin homology <CYS>
F;131-148/Product: protegrin 4 #status predicted <NMID:
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT: P49934; UNIPARC: UPI0000131779; EMBL; X84096; NID: g887646; PID
A; Experimental source: leukocytes
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F;30-130/Domain: propeptide #status predicted <PRO>
F;131-148/Product: protegrin 5 #status predicted <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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SSTOUT 12
SSTOOP
Protegrin 5 precursor - pig
NrAlternate names: cathelin-associated antimicrobial peptide
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S66203; SST609
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 369, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                      C;Genetics:
A;Gene: NPG5
A;Introns: (6/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial
C;Keywords: amidated carboxyl end; antibacterial
F;1-29/Domain: signal sequence #status predicted <SIG>
                                                                                                    QOSPEDCDPKKDGLVKRCMGTVTLNQARGSPDISCDK 97
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Best Local Similarity
Matches 64; Conserva
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Best Local Similarity
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A;Reference number: S41731; MUID:94123775; PMID:8293820
A;Accession: S41731
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-166 <STO>
A;Cross-references: UNIPROT:P49931; UNIPARC:UPI000012F428; GB:L29125; NID:9457347; PIDN:C;Superfamily: cathelin; cystatin homology
F;22-129/Domain: cystatin homology <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18K lipopolysaccharide-binding protein precursor - rabbit
N.Alternate names: 18K cationic protein
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Saccesion: 301171; PS0226
R.Larrick, J.W.; Morgan, J.G.; Palings, I.; Hirata, M.; Yen, M.H.
B.Jochen: Blophys. Res. Commun. 179, 170-175, 1991
A.Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding
A.Accession: JQ1171; WJID:91354246; PMID:1883348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.R.Cogule type: mRNA
A.Residues: 1-171 < LAR>
A.Residues: 1-171 < LAR>
A.Experimental source: bone marrow
A.Accession: PS0226
A.Molecule type: protein
A.Residues: 135-159, 'QIGQLL' < LAZ>
A.Coss-references: UNIPARC:UP10000176372
A.Note: 157-Asp was also found
A.Note: 157-Asp was also found
C.Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <NMT>
                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTHMDGDPDTPKPVSFTVKETVCPRTT 60
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; Pred. No. 1.1e-29;
13; Mismatches 19; Indel8
                                                                                                                                                                                                                                                                                            Query Match 64.3%; Score 344; DB 2; Length 166; Best Local Similarity 66.0%; Pred. No. 8.3e-30; Matches 64; Conservative 15; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 67.0%;
Matches 65; Conservative 1
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90 WKLPEQCDFKEDGLVKRCVGTVTRYQAMDSFDIRCNR 126 61 QQSPEDCDFXXDGLVRCMGTVTLNQARGSFDISCDK 97 ò

Search completed: January 12, 2006, 21:51:07 Job time : 8.94465 secs

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Gaps ö 1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTWDGDPDTPKPVSFTVKBTVCPRTT 60

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pt 1+22

GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.

January 12, 2006, 21:42:24 ; Search time 49.1956 Seconds (without alignments) 1448.471 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-815-562-2_COPY_31_131 535 1 QVLSYKGAVLRAIDGINQRS......VTLNQARGSFDISCDXDNKR 101 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 segs, 705528306 residues Searched:

2166443 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	P49913 homo sapien		Q9glv5 macaca mula	O62841 equus cabal		P54230 ovis aries	O62840 equus cabal		P82018 capra hircu	P79362 ovis aries	Q4jfb9 capra hircu	P22226 bos taurus	P54229 bos taurus	BNB	P51524 sus scrofa	P32195 sus scrofa	P32194 sus scrofa	P32196 sus scrofa	P49933 sus scrofa	8118		P49931 sus scrofa		P25230 oryctolagus	P49928 ovis aries	P49932 sus scrofa	P19660 bos taurus	P56425 bos taurus	P54228 bos taurus	Q9xsq8 capra hircu	P49929 ovis aries
SUMMAKIES		QI .	PAL39 HUMAN	FAL39_MACMU	Q9GLV5_MACMU	O62841_HORSE	O62842_HORSE	BCTN1 SHEEP	062840 HORSE	PMP23 PIG	BCTN5 CAPHI	BCTN5_SHEEP	Q4JFB9 CAPHI	BCTN1 BOVIN	BMA28_BOVIN	PR39_FIG	PP11_PIG	PG2_FIG	PG1_PIG	PG3_PIG	PG4_PIG	PG5_PIG	PF12 PIG	PMP36 PIG	Q71KM5 RAT	CAP18 RABIT	SCS1 SHEEP	PMP37 PIG	BCTN5_BOVIN	BMA34_BOVIN	BMA27 BOVIN	Q9XSQ8 CAPHI	SC52_SHEEP
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		Match Length DB	170	170	170	157	170	155	156	153	176	176	176	155	159	172	212	147	149	149	149	149	228	166	171	171	160	167	176	165	158	158	160
	Query	Match	100.0	100.0	94.0	75.0	9.89	68.4	68.0	67.5	67.5	67.5	67.5	66.2	62.9	65.4	65.4	64.9	64.9	64.9	64.9	64.9	64.7	64.3	64.3	64.1	63.6	63.6	63.6	63.5	63.3	62.4	62.3
		Score	535	535	503	401	367	366	364	361	361	361	361	354	352.5	350	350	347	347	347	347	347	346	344	344	343	340.5	340	340	339.5	338.5	334	333.5
	Result	No.	г	8	e	4	S	9	7	80	on	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31

P19661 bos taurus Qétn20 canis famil P51437 mus musculu Q683r8 bubalus bub P33046 bos taurus P15175 sus scrofs P79361 cvis aries P79360 cvis aries P59415 cvis aries P50415 cvis aries P62017 capra hircu P79360 cvis aries P50415 cvis aries P62017 capra hircu P79360 cvis aries P62017 capra hircu Q19041 cvis aries	e update) ion update) ion update) iursor (FALL-39 peptide antibiotic) iursor (FALL-39 peptide antibiotic) iurata; Vertebrata; Buteleostomi; is, Primates; Catarrhini; Hominidae; antibiotic, is cysteine-free and s."; antibiotic, is cysteine-free and s."; boll-199(1995). ioTEIN SEQUENCE OF 42-68 AND 83-100. DOI=10.1016/0014-5793(95)00634-L; faard N.; n-like protein of human neutrophillike protein of theman caphil prancke U., Wright S.C.; Francke U., Wright S.C., Francke U., Wright S.C.,	Bergman T., Olsson B.,
190 1 BCTN7 BOVIN 172 2 G6TN2 ⁷ CANPA 173 1 CRAMP MOUSE 144 2 0663R6 BUBBU 144 1 100C_BOVIN 96 1 ICTL PIG 164 2 P793 ⁶ LSHERP 190 2 Q9XSQ9_CAPHI 165 2 P793 ⁶ GHERP 190 1 BCTN7 SHERP 190 1 BCTN7 SHERP 165 2 P82017 CAPHI 162 2 P82017 CAPHI 162 2 P82017 CAPHI 163 2 019040_SHERP 178 2 Q91X12_CAVPO	HUMAN FALSA HUMAN OLOCT-1996 (Rel. 34, Last sequence update) 13-SEP-2005 (Rel. 34, Last sequence update) Antibacterial protein LL-37) Human-CAPIS Syndyman CORITORIA SACONAMA CORITORIA SURVEY MARMADIA BURCHETIA BUARCHORICGINES PRIMATESIS OF 132-170. NCBI TEXISPESON GH; NUCLEOTIOR SEQUENCE (MENNA), AND SYNTHESIS OF 132-170. MUCLEOTIOR SEQUENCE (MENNA), AND FORTEIN SEQUENCE OF 42-68 AND 83-100. MUCLEOTIOR SEQUENCE (MENNA), AND PROTEIN SEQUENCE OF 42-68 AND 83-100. MUCLEOTIOR SEQUENCE (MENNA), AND PROTEIN SEQUENCE OF 42-68 AND 83-100. MUCLEOTIOR SEQUENCE (MENNA), AND PROTEIN SEQUENCE OF 42-68 AND 83-100. MUCLEOTIOR SEQUENCE (MENNA), AND PROTEIN SEQUENCE OF 42-68 AND 83-100. MUCLEOTIOR SEQUENCE (MENNA), AND PROTEIN SEQUENCE OF 42-68 AND 83-100. MUCLEOTIOR SEQUENCE (MENNA), AND PROTEIN SEQUENCE OF 42-68 AND 83-100. MUCLEOTIOR SEQUENCE (MENNA), AND PROTEIN SEQUENCE OF 42-68 AND 83-100. MUCLEOTIOR SEQUENCE (MENNA). 13	ic DNA]. h B., Odeberg J.,
23 333 62.2 14 327 62.1 15 324 60.6 16 323 60.4 17 312 59.4 18 318 59.4 19 316 59.4 11 312 58.3 12 303.5 14 299 55.9	HUMAN 49913; 1-0CT-1996 (Rel. 3 1-0CT-1996 (Rel. 3 1-0CT-1996 (Rel. 3 3-SEP-2005 (Rel. 4 ntibacterial protection on the control of the	SEQUENC 1941; n G.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                 Halleck A., Ebert L., Mkoundinya M., Schick M., Elsenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Korn B., Zuo D., Hu Y., LaBaer J., "Cloning of human full open reading frames in Gateway (TM) system entry vector (pDONR201)."; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
"The human gene PALL39 and processing of the cathelin precursor to the antibacterial peptide LL-37 in granulocytes.", Bur. J. Biochem. 238:325-332(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibacterial activity.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Expressed in bone marrow and testis and
                                                                                                                                                                     Wu N., Mao S.Y., Zhang X.D., Qiao Y., Liang G., Wang L.F., "A new spermatogenesis-related gene.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                             Gao Y., Huang Y.F., Xia X.Y.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: The N-terminus is blocked.
SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Z38026; CAA86115.1; -; mRNA.

EMBL; X89658; CAA61805.1; -; mRNA.

EMBL; U19970; AAA74084.1; -; mRNA.

EMBL; U48795; AAC02634.1; -; Genomic_DNA.

EMBL; X96735; -; NOT_ANNOTATED_CDS; Genomic_DNA.

EMBL; AX251531; AAN76318.1; -; mRNA.

EMBL; AX251531; AAP20054.1; -; mRNA.

EMBL; CR457083; CAG33364.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ensembl; ENSG0000164047; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR541961; CAG46759.1; -; BC055089; AAH55089.1; -;
                                                              NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                           NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; I38932; I38932.
PIR; S74248; S74248.
                                                                                TISSUE-Epididymis;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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By similarity.

D -> N (in Ref. 1, 6, 7 and 8; CAG46759).

055B07DCA95A7D16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last sequence update)
Antibacterial protein FAL-39 precursor (FALL-39 peptide antibiotic)
(Cationic antimicrobial protein CAP-18) (rhCAP-18) [Contains:
Antibacterial protein LL-37 (rhLL-37)].
Name=CAMP; Synonyme=CAP18, FALLS9;
Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Butelcostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae, Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
NUCLEOTIDE SEQUENCE [MENA], AND TISSUE SPECIFICITY.
NUCLEOTIDE SEQUENCE [MENA], AND TISSUE SPECIFICITY.
NUCLEOTIDE STATE 11239624; DOI=10.1128/CDLI.8.2.370-375.2001;
Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
Rhesus monkey (Macaca mulatta) mucosal antimicrobial peptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           close homologues of human molecules.";
Clin. Diagn. Lab. Immunol. 8:370-375(2001).
-1- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                             Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 535; DB 1; Length 170; 100.0%; Pred. No. 7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                         Antibacterial protein FALL-Antibacterial protein LL-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 QOSPEDCDFYKCOGLVYRCKGTVTLNQARGSFDISCDKDNKR 131
                                                                    Pram; PP00666; Cathelicidins; 1.
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Direct protein sequencing; Pyrrolidone carboxylic acid; Signal.
SIGNAL
GO; GO:0042742; P:defense response to bacteria; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Bimilarity
                      InterPro; IPR001894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 AA; 19301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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134
31
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30 QTLSYKEAVLRAVDGLNQRSSDENLYRLLELDPLPKEDEDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone marrow;
MEDINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Glulotto E.,
Zanetti M.;
                                                                                                                                                                                                                                                                                                      TISSUE=Bone marrow;
MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OG2842_HORSE PRELIMINARY; PRT; 170 AA.
062842_
062842_
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 24, Last sequence update)
01-AUG-1998 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Myeloid cathelicidin 3 precursor.
Name=eCATH-3;
Equus caballus (Horse).
Equus caballus (Horse).
Equus caballus (Horse).
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                    Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E., Zanetti M.;

"Novel cathelicidins in horse leukocytes.";

FEBS Lett. 457:459-464(1999).

EMBL; AJ224928; CAA12227.1; -; mRNA.

HSSP; P32196; INVI.

SMR; O62841; 30-130.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0005578; P:eafense response; IEA.
GO; GO:0009613; P:response to pset, pathogen or parasite; IEA.
InterPro; IPR001984; Cathellcidin.
ProDom: PF00666; Cathellcidins; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          myeloid cathelicidin 2.
1424C493D2B307CC CRC64;
   91 QKSPEDCDFKEDGLVKRCVGTVILNQARDSFDISCDKDNRR 131
                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.0%; Score 401; DB 2; 77.3%; Pred. No. 1.3e-34; tive 10; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Novel cathelicidins in horse leukocytes.";
                                                                                   157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
                                                                                   PRT;
                                                                                                                    Created)
                                                                                                                                                                     Myeloid cathelicidin 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18153 MW;
                                                                                                                    01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75; Conservative
                                                                                   O62841 HORSE PRELIMINARY;
O62841;
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157
                                                                                                                                                                                   Name=eCATH-2;
Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
30
157 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 QVLSYQEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 90
                                                                                                                                                                                                                                                                                                                                       1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOI=10.1128/AAC.45.10.2695-2702.2001;
Zhao C., Nguyen T., Boo L.M., Hong T., Espiritu C., Orlov D., Wang W., Waring A., Lehrer R.I.;
"RL-37, an alpha-helical antimicrobial peptide of the rhesus monkey.";
Antimicrob. Agents Chemother. 45:2695-2702(2001).
EMBL; AF181954; AAG09440.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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Macaca mulatta (Rhesus macaque).

Macaca mulatta; Metacos; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Cercopithecidae; Cercopithecinae; Macaca.
EMBL, AF288284, AAG40802.1; -; mRNA.
InterPro; IPR001894; Cathelicidin.
PANTHERS, PTHR10206; Cathelicidin; 1.
Pfam; PF00666; Cathelicidins; 1.
Probom, PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
SIGNAL 1 30 Potential.
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GO; GO:000652; P:defense response; IEA.
GO; GO:0006913; P:response to pest, pathogen or parasite; IEA.
InterPro; IPRO01894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
ProDom; PD001839; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
SEQUENCE 170 AA; 18861 MM; 355AB3BF510DBB83 CRC64;
                                                                                                                                                                   Antibacterial protein PALL-39.
Antibacterial protein LL-37.
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                       100.0%; Score 535; DB 1; Length 170; 100.0%; Pred. No. 7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 503; DB 2; Length 170; Pred. No. 1.8e-45; 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                     055B07DCA95A7D16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            91 QOSPEDCDPKGGGLVKRCMGTVTLNQARGSPDISCDKONKR 131
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                                                                                                                                                                                                                                                                                                                                                                                                           61 QQSPEDCDFKKDGLVKRCMGTVTLNQARGSPDISCDKDNKR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 AA
                                                                                                                                                                                                                                                                                                        0; Mismatches
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MEDLINE-21441139; PubMed=11557457;
                                                                                                                                                                                                                                       170 AA; 19301 MW;
                                                                                                                                                                                                                                                                                        100.08;
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94; Conservative
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                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 101, Conservative
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Matches 94; Conserv
                                                                                                                                                                                                                                       SEQUENCE
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30 QVLSYREAVLRAVDQLMEQSSEPNIYRLLELDQPPQDDEDPDSPKRVSFRVKETVCPRTT
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MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Perissodactyla; Equidae; Equus
                        PIR; S68229; S68229.

HISSP, P32196; IKWI.

SMR; P54230; 30-130.

InterPro; IPRO1894; Cathelicidin.

PANTHER; PTHR10206; Cathelicidin; 1.

Prom; PP00066; Cathelicidin; 1.

PROSITE; PS00946; CATHELICIDINS 1; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

Anthiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.

SIGNAL.
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GO; GO:0005576; C:extracellular region; IEA.
GO; GO:000551; P:defense response; IEA.
GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
InterPro; IPR001894; Cathelicidin.
ProDom; PF001666; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 1; 1.
                                                                                                                                                                                                                                                                                                                                        By similarity.
Cyclic dodecapeptide.
Pyrrolidone carboxylic acid (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.4%; Score 366; DB 1; Length 155; 69.8%; Pred. No. 6.8e-31; ive 16; Mismatches 13; Indels
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Potential.
BB8EASD150288FFD CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 QQPPEQCDFKENGLLKRCEGTVTLDQVRGNFDITCN 125
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Pred. No. 1.1e-30;
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By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zanetti M.;
"Novel cathelicidins in horse leukocytes.";
PEBS Lett. 457;459-464(1999).
EMBL; AJZ24927; CAA12226.1; -; mRNA.
HSSP; P32196; 1KWI.
SWR; O62840; 30-130.
EMBL; U60596; AAB49711.1; -; Genomic_DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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O62840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67; Conservative
                                                                                                                                                                                                                                                                                                                                                          143
155
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124
154
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Equus caballus (Horse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QVLSYKGAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-98121317; PubMed-9461419; DOI-10.1016/S0378-1119(97)00569-6; Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.; "Localization and genomic organization of sheep antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Bone marrow;
MEDLINE=96105386; PubMed=7498547; DOI=10.1016/0014-5793(95)01285-3;
Bagella L., Scocchi M., Zanetti M.;
"CDNA sequences of three sheep myeloid cathelicidins.";
PEBS Lett. 376:225-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Covis aries (Sheep).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalla; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 206:85-91(1998).
-!- FUNCTION: Potent microbicidal activity, active against
-!- Staphylococcus aureus and Escherichia coli (By similarity).
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                        SMR; O62842; 30-130.

GO; GO:0005576; C:extracellular region; IEA.

GO; GO:0006952; P:defense response; IEA.

GO; GO:0006913; P:response to pest, pathogen or parasite; IEA.

InterPro; IPR001894; Cathelicidin.

Pfam; PF00666; Cathelicidins; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 68.6%; Score 367; DB 2; Length 170; Local Similarity 68.0%; Pred. No. 5.9e-31; les 68; Conservative 13; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    myeloid cathelicidin 3. 5C35F1FA2D112BC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
13-SRP-2005 (Rel. 48, Last annotation update)
Cyclic dodecapeptide precursor (Bactenecin 1) (Bacl).
Name=BACIA; Synonyms=DODEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L46853; AAA85469.1; -; mRNA.
EMBL; U60595; AAB49710.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                            Potential.
                                                                                                                                                                                                                                                                  Prodom, PD001838; Cathelicidin, 1.
PROSITE, PS00946; CATHELICIDING 1, 1.
PROSITE; PS00947; CATHELICIDING 2, 1.
      FEBS Lett. 457:459-464(1999).
EMBL; AJ224929; CAA12228.1; -; mENA.
HSSP; P32196; 1KWI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                    30 170 m
170 AA; 19299 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=BAC1B; Synonyms=DODEB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHEEP
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SIGNAL
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Similarity
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107
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Best Local &
Matches 66
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                                            Zhao C., Lehrer R.I.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Exerts antimicrobial activity against both Gram-positive and negative bacteria at concentrations of 2-16 micro molar. Its activity appears to be mediated by its ability to damage bacterial
                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial peptide PMAP-23 precursor (Myeloid antibacterial peptide
                            QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
 Gaps
                                                                                                                                                                                                                                                                                              Namestrano...
Sus acrofa (Pig).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mommalia: Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Bone marrow;
MEDLINE=94179144; PubMed=8132502;
Anabtin M., Storici P., Tossi A., Scocchi M., Gennaro R.;
Anolecular cloning and chemical synthesis of a novel antibacterial peptide derived from pig myeloid cells.";
J. Blol. Chem. 269:7855-7858 (1994).
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SMR; P49930; 30-130.
InterPro; IPR01894; Cathelicidin.
PANTHER; PTHA10206; Cathelicidin; 1.
ProDom; P0001838; Cathelicidin; 1.
ProDom; P0001838; Cathelicidin; 1.
PROSITE; P800946; CATHELICIDINS 1; 1.
PROSITE; P800947; CATHELICIDINS 2; 1.
Antiblotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibacterial peptide PMAP-23. Pyrrolidone carboxylic acid (E
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7ADAA22B6C206000 CRC64;
                                                                                                  90 KQTPEQCDFKENGLVKQCVGTVILGPVKDHFDVSCGEPQR 129
                                                                                   QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the cathelicidin family.
20;
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                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 131-153
                                                                                                                                                                                      153 AA
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By similarity.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L26053; AAA31103.1; -; mRNA.
EMBL; Y16624; CAA76328.1; -; Genomic_DNA.
PIR; A53421; A53421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
13;
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Conservative
                                                                                                                                                                                     STANDARD;
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124
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                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                      Name=PMAP23;
                                                                                                                                                                                     PIG
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                                                         30 QALSYREAVLRAVDRINEQSSEANLYRLILELDQPPKADEDPGTPKPVSFTVKETVCPRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTWDGDPDTPKPVSPTVKETVCPRTT
                                                                                                                                                                                                                                                                                             Capra hirous (Goat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE OF 131-149 AND 151-153, AND PROTEIN SEQUENCE. TASSURE-BOOM marrow, and Leukocyte, MEDLINE=99346202; PROMED=1047180; Shamova O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P32196; 1KWI.

SMR; P82018; 30-130.

InterPro; PRO0189; Cathelicidin.

PANTHER; PTHR10206; Cathelicidin; 1.

Probom; P0001838; Cathelicidin; 1.

PROSITE; P800947; CATHELICIDINS 1; 1.

PROSITE; P800947; CATHELICIDINS 2; 1.

PROSITE; P800947; CATHELICIDINS 2; 1.

PROFICE; PRODICE; Antimicrobial; Direct protein sequencing; Pyrrolidone carboxylic acid; Repeat; Signal.

SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrrolidone carboxylic acid (By
             14; Indels
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6PD7056C954B340A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: Blastase is responsible for its maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bactenecin 5.
Removed in mature form
                                                                                                             61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
68.0%; Pred. No. 2.3e-30; ive 17; Mismatches 14
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    group).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
13-SEP-2005 (Rel. 48, Last annotation
Bactenecin 5 precursor (Bac5) (ChBac5)
                                                                                                                                                                                                                                                                                                                                         Pecora; Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19846 MW;
             66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96
124
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DISULPID
SEQUENCE
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Capra hircus (Goat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Bone marrow;
                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                        protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=BAC1;
                                                                                                                                                                                                                                                                                   Name=bac5;
CONFLICT
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                                                                                                                                                                                                   39 CAPHI
Q4JFB9_C
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                                                          Matches
                                                                                                                                                                                     RESULT 11
Q4JFB9_CAE
                                                                                                                                                                                                                                                                          Bacs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao
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                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98121317; PubMed=9461419; DOI=10.1016/S0378-1119(97)00569-6; Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.; "Localization and genomic organization of sheep antimicrobial peptides
                                                                        30 OALSYREAVLRAVGOLNERSSEANLYRLLELDPAPNDEVDPGTRKPVSFTVKETVCPRTT
                                                           1 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- PTM: Blastase is responsible for its maturation (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
                                                                                                                                                                                                                                                          Name=BAC5;
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                      genes";

Gene 206:85-91(1998).

Gene 206:85-91(1998).

Inpipolysaccharides (LPS), a glycolipid present in the outer membrane of all Gram-negative bacteria. Potent antimicrobial activity (By similarity).

DOMAIN: BACS sequence consists almost exclusively of X-P-P-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biminarity/.
Proline amide (G-174 provides amide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrrolidone carboxylic acid (By
            Query Match 67.5%; Score 361; DB 1; Length 176; Best Local Similarity 68.0%; Pred. No. 2.7e-30; Matches 66; Conservative 17; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Removed in mature form.
                                                                                                                     90 QQPPEECDFKENGLVKQCVGTVTLDPSNDQFDINCNE 126
                                                                                                       61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
                                                                                                                                                                                                P79362; P79363;
10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Bactenecin 5 precursor (Bac5) (OaBac5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              group).
By similarity.
By similarity.
                                                                                                                                                                                         PRT; 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bactenecin 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U60599; AAB49714.1; -; Genomic_DNA
EMBL; U60601; AAB49716.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P32196; 1KWI.

EMR; P79362; 30-130.

InterPror; IPR001994; Cathelicidin.

PANTHER, PTR10206; Cathelicidin; 1.

Pfam; PF00666; Cathelicidins; 1.

PROSITE; PS00946; CATHELICIDINS; 1.

PROSITE; PS00947; CATHELICIDINS; 1.
                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE (GENOMIC DNA / MRNA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
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                                                                                                                                                                                          STANDARD;
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130
173
176
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124
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174
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107
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                                                                                                                                                                                                                                                                                                                                                         TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeats.
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                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification and properties of proline-rich antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Capra.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.5%; Score 361; DB 2; Length 176; Best Local Similarity 68.0%; Pred. No. 2.7e-30; Matches 66; Conservative 17; Mismatches 14; Indels
                                                                            Length 176;
79 79 T -> R (in Ref. 1; AAB49716).
176 AA; 19842 MW; 05080026EA6FD5F7 CRC64;
                                                                                                                                   14; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; Y18873; CAC80206.1; -; mRNA.
SEQUENCE 176 AA; 19846 MW; 6FD7056C954E340A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Bac1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                           90 QOPPEECDFKENGLVKQCVGTVTLDPSNDQFDINCNE 126
                                                                                                                                                                                                                                                                                               61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
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                                                                            ; Score 361; DB 1;
; Pred. No. 2.7e-30;
17; Mismatches 14;
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01-OCT-1993 (Rel. 27, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Cyclic dodecapeptide precursor (Bactenecin 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Bone marrow;
MEDLINE=99346202; PubMed=10417180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from sheep and goat leukocytes.";
Infect. Immun. 67:4106-4111(1999)
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                                                                                  67.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04JFB9;
04JFB9;
13-SEP-2005 (TYEMBLYEL: 31,
13-SEP-2005 (TYEMBLYEL: 31,
13-SEP-2005 (TYEMBLYEL: 31,
                                                                                                                                      66; Conservative
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                                                                              This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                      MEDLIRE=96300243; PubMed=8706679; Storici P., Tossi A., Lenarcic B., Romeo D.; Storici P., Tossi A., Lenarcic B., Romeo D.; Purification and structural characterization of bovine cathelicidins, precursors of antimicrobial peptides."; Eur. J. Biochem. 238:769-776(1996).
-!- FUNCTION: Potent microbicidal activity, active against Staphylococcus aureus and Escherichia coli.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Large granules of neutrophils.
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 QALSYREAVLRAVDQLNEQSSEPNIYRLLELDQPPQDDEDPDSPKRVSFRVKETVCSRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                         MEDLINE-88257074; PubMed=3290210;
Romeo D., Skerlavaj B., Bolognesi M., Gennaro R.;
"Structure and bactericidal activity of an antibiotic dodecapeptide purified from bovine neutrophils.";
J. Biol. Chem. 263:9573-9575(1988).
                                 IISSUE=Bone marrow;
MEDLINE=93093170; PubMed=1459251; DOI=10.1016/0014-5793(92)80971-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                      Storici P., del Sal G., Schneider C., Zanetti M.; "CDNA sequence analysis of an antibiotic dodecapeptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclic dodecapeptide.
Pyrrolidone carboxylic acid.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P32196; IKMI.

HSSP, P32196; IKMI.

INCEMPORT P2226; 30-130.

INCEMPORT P2226; 30-130.

INCEMPORT P2226; 30-130.

PANTHER; PTRE10206; Cachelicidin; 1.

ProDom, P0001838; Cathelicidin; 1.

PROSITE; PS00946; CATHELICIDINS 1; 1.

PROSITE; PS00947; CATHELICIDINS 2; 1.

Antiblocic; Antimicrobial; Direct procein sequencing; Pyrcolidone carboxylic acid; Signal.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
                                                                                                                                   Scocchi M., Wang S., Zanetti M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q -> R.
008CD7DC6CB91BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.2%; Score 354; DB 1; 67.7%; Pred. No. 1.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.7%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L08834; AAA50615.1; -; mRNA.
EMBL; Y09472; CAA70617.1; -; Genomic_DNA.
PIR; S27018; S27018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17600 MW;
                                                                                       'EBS Lett. 314:187-190(1992)
                                                                                                                                                                      PROTEIN SEQUENCE OF 144-155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
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124
154
154
                       NUCLEOTIDE SEQUENCE.
                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 AA;
                                                                                                                                                                                 rissum=Neutrophil;
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Les 65, Conserv
                                                                                                                                                                                                                                                               CHARACTERIZATION.
NCBI_TaxID=9913;
                                                                                                                           TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDE
MOD_RES
DISULPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT
SEQUENCE
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Matches
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01-OCT-1996 (Rel. 34, Last sequence update)
13.5EP-2005 (Rel. 48, Last annotation update)
Antibacterial peptide BMAP-28 precursor (Myeloid antibacterial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96300243; PubMed=8706679; Storici P., Tossi A., Lenarcic B., Romeo D.; Storici P., Tossi A., Lenarcic B., Romeo D.; Storici P., Tossi A., Lenarcic B., Romeo D.; precursors and structural characterization of bovine cathelicidins, precursors of antimicrobial peptides."; Eur. J. Blochem. 238:769-776(1996).

-I- FUNCTION: Exerts a potent antimicrobial activity against Gramnegative and Gram-positive bacteria, including methicillin-resistant Staphylococcus aureus, and fungi.

-I- MASS SPECTROMERRY: MW-4141; MW_ERR=1; METHOD=Electrospray; RANGE=30-159; NOTE=Ref.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGD-PDTPKPVSFTVKETVCPRT
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                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Biological characterization of two novel cathelicidin-derived peptides and identification of structural requirements for their antimicrobial and cell lytic activities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Bone marrow;
MEDLINE=97067059; PubMed=8910461; DOI=10.1074/jbc.271.45.28375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X97609; CAA66208.1; -; mRNA.
HSSP; P32196; 1KWI.
SWR; P54229; 30-131.
SWR; P54229; 30-131.
PANTHER; PTHR01894; Cathelicidin.
Probon; P001838; Cathelicidin; 1.
Probon; P001838; Cathelicidin; 1.
PROSITE; P800946; CATHELICIDINS 1.
PROSITE; P800947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cathelicidin-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 65.9%; Score 352.5; DB 1; Length 159; Local Similarity 67.7%; Pred. No. 1.9e-29; les 65; Conservative 17; Mismatches 13; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skerlavaj B., Gennaro R., Bagella L., Merluzzi L., Risso A.,
Zanetti M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibacterial peptide BMAR-28 Pyrrolidone carboxylic acid. By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BMAP-28
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89B7CB46C5EEC367 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the cathelicidin family.
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                                                                                                                                                               159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem. 271:28375-28381(1996).
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17616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pecora; Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                               STANDARD;
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  30 QALSYREAVLRAVDQLNEKSSEANLYRLLELDPPPKEDDENPNIPKPVSFRVKETVCPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUR=Neutrophil; white a second of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95350216; PubMed=7624374; Gudmundsson G.H., Magnusson K.P., Chowdhary B.P., Johansson M., Andersson L., Boman H.G.; Extraction of the gene for porcine peptide antibiotic PR-39, a cathelin gene family member: comparative mapping of the locus for the human peptide antibiotic PALL-39."; Proc. Natl. Acad. Sci. U.S.A. 92:7085-7089(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Anino acid sequence of PR-39. Isolation from pig intestine of a new member of the family of proline-arginine-rich antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Liver;
MEDLINE=96105365; PubMed=7498526; DOI=10.1016/0014-5793(95)01237-3;
Zhao C., Ganz T., Lehrer R.I.;
"Structures of genes for two cathelin-associated antimicrobial
peptides: prophenin-2 and PR-39.";
FEBS Lett. 376:130-134(1995).
                                                                                                                                                                                                                                                                                                         Name=PR39;
Sus acrofa (P1g).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the small intestine.";
J. Leukoc. Biol. 56:807-811(1994).
-!- FUNCTION: Exerts a potent antimicrobial activity against both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Storici P., Zanetti M.;
"A cDNA derived from pig bone marrow cella predicts a sequence
interioral to the intestinal antibacterial peptide PR-39.";
Blochem. Biophys. Res. Commun. 196:1058-1065(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Intestine;
MEDLINE=92111534; PubMed=1765098;
Agerberth B., Lee J.-Y., Bergman T., Carlquist M., Boman H.G.,
Mutt V., Joernvall H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E.coli and B.megaterium.
--- TISSUE SPECIFICITY: Small intestine and bone marrow.
---- SIMILARITY: Belongs to the cathelicidin family.
                                                            90 SQQSPEQCDFKENGLLKECVGTVTLDQVGSNFDITC 125
                                         60 TOOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISC 95
                                                                                                                                                                                                    P80054; Q9TR84;
01-MAR-1992 (Rel. 21, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
Antibacterial protein PR-39 precursor.
                                                                                                                                                                                    PRT; 172 AA
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MEDLINE=94071853; Pubmed=8250863;
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MEDLINE=96042752; PubMed=7576250;
MEDLINE=96042752; PubMed=7576250;
MEDLINE=96042752; PubMed=7576250;
MEDLINE=96042762; PubMed=7576250;
MEDLINE=9604762; Turk V.;
Molecular cloning and identification of a novel porcine cathelin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 QALSYREAVLRAVDRLNEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCFRPT
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MEDLINE=95212585; PubMed=7698355; DOI=10.1016/0014-5793(95)00210-Z;
Harwig S.S.L., Kokryakov V.N., Swiderek K.M., Aleshina G.M., Zhao C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-0CT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Prophenin-1 procursor (PF-1) (C6) (Fragment).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proline amide (G-170 provides amide
                                                                                                                                                                               Pfam; Pro0666; Cathelicidin; 1.
Problom; PP00666; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Amidation; Antibiotic; Antimicrobial; Direct protein sequencing; Pyrrolidone carboxylic acid; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial protein PR-39. Pyrrolidone carboxylic acid (By similarity).
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; Pred. No. 3.9e-29;
15; Mismatches 16; Indels
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124 By similarity.
21 G -> A (in Ref. 2).
29 A -> T (in Ref. 1).
91 RQ -> QR (in Ref. 1).
119 IMS -> NDP (in Ref. 1).
157 P -> I (in Ref. 5).
157 P -> I (in Ref. 5).
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EMBL, X87236; CAA60682.1; -; Genomic_DNA.
EMBL, L23825; AAA31109.1; -; mRNA.
EMBL, X89201; CAA61487.1; -; Genomic_DNA.
PIR; S68222; S68232.
HSSP, P32196; IKWI.
SMR; P80064; 30-130.
InterPro; IPR001894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
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Biol. Chem. Hoppe-Seyler 376:507-510(1995)
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Matches 66; Conservative
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.ehrer R.I.; Prophenin-1, an exceptionally proline-rich antimicrobial peptide from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QALSYREAVLRAVDRINEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCPRPT
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R PIR; S57330; S57330
R HSSP; P32136; Land.
R HSSP; P32136; Land.
R InterPro; IPR001894; Cathelicidin.
R PAWTHER; PTHR.0206; Cathelicidin; 1.
R ProDom; PD001838; Cathelicidin; 1.
R PROSITE; PS00946; CATHELICIDINS_1; 1.
R PROSITE; PS00947; CATHELICIDINS_2; 1.
                                porcine leukocytes.";
FEBS Lett. 362:65-69(1995).
-!- FUNCTION: Exerts antimicrobial activity. It is more effective against Gram-negative bacteria than Gram-positive bacteria.
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrrolidone carboxylic acid (By similarity).
Proline amide (G-210 provides amide group) (Potential).
By similarity.
By similarity.
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Prophenin-1.
Removed in mature form (Potential).
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1 QVLSYKEAVLRAIDGINQRS......VTLNQARGSFDISCDKDNKR 101
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GenCore version 5.1.6
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US-08-243-819A-38
US-08-243-819A-40
US-08-243-879A-40
US-08-243-879A-40
US-08-243-879A-40
US-08-243-879A-40
US-08-243-879A-40
US-08-243-879A-40
US-09-128-345-6
US-08-499-523-8
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Listing first 45 summaries
                                              - protein search, using sw model
                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                seq length: 0
seq length: 200000000
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Match Length
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Perfect score:
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364
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347
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Maximum DB
                                              OM protein
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                                                                      Run on:
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No.
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Sequence 4, Appli Sequence 36, Appl Sequence 5, Appli Sequence 5, Appli Sequence 1180, Ap Sequence 1180, Ap Sequence 10, Appl Sequence 10, Appl Sequence 3, Appli Sequence 3, Appli	Encoded Human Proteins.	Length 152; Indels 0; Gaps 0; DDTPREVSFTVKBTVCPRTT 60	би:
171 2 US-09-322-911-4 160 2 US-09-917-340-36 176 2 US-09-917-340-28 96 2 US-09-313-681A-5 96 2 US-09-322-911-5 18 2 US-09-322-911-5 18 2 US-09-385-328-10 18 2 US-09-386-328-10 18 10 2 US-09-568-486-3	ALIGNMENTS 3, J.B. Sequence Tags and 249/513,999C 240/122,487	100.0%; Score 535; DB 2; Length 152; imilarity 100.0%; Pred. No. 7e-60; conservative 0; Mismatches 0; Indele 0; Gaps QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTT QQSPEDCDFKKDGLVKRCMGTVTLNQARGSPDISCDKDNKR 101	. US/08313681A James W. Susan C. Mishimasa Human Cationic Proteins Having
28 343 64.1 12 29 340.5 63.6 13 34 35 63.6 13 32 325 60.7 32 60.7 32 32 32 60.7 34 35 126 23.6 126 23.	RESULT 1 US-09-513-999C-7862 Sequence 7862, Application US/09 GENERAL INFORMATION: APPLICANT: Duclett, A. TITLE OF INVENTION: Expressed S. PATENT OF 100-16-11, APPLICANT: TITLE OF INVENTION UNMER: US/CURRENT PLING DATE: 2000-02-2 CURRENT FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOOTWARE: PATENTION NUMBER: US/CURRENT PLING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SEQ ID NO 7662 LENGTH: 152 TYPE: PT ORGANISM: Homo sapiens FRATURE: COCATION: -1331 OTHER INFORMATION: SCOFE 9.5 COTHER INFORMATION: SCOFE 9.5 COTHER INFORMATION: SCOFE 9.5	Query Match Best Local Similarity 100 Matches 101; Conservative Qy 1 QVLSYKEAVLRAIDG Db 34 QVLSYKEAVLRAIDG Qy 61 QQSPEDCDFKKDGIV Db 94 QQSPEDCDFKKDGIV Db 94 QQSPEDCDFKKDGIV	RESULT 2 US-08-313-681A-2 Sequence 2, Application US/08 Patent No. 5618675 GENERAL INFORMATION: APPLICANT: Larrick, James APPLICANT: Wright, Susan APPLICANT: Wright, Susan TITLE OF INVENTION: Human

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US-09-917-340-32
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APPLICANT: Wright, Susan C.
APPLICANT: Wright, Susan C.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata Mishimasa
APPLICANT: Balint, Robert W.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity NUMBER OF SEQUENCES: 30
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                         NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
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                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYRE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/313,681A

FLING DATE:

CLASSIFICATION: 435

ATTORNEY AGENT INFORMATION:

NAME: Healin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 29,541

REPERENCE/DOCKET NUMBER: 29,541

REPERENCE/DOCKET NUMBER: 15325-9-1

TELEPHONE: 415-326-2420

TELEPHONE: 415-326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 170 amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: ADDIACY: 1 inear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
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MOLECULE TYPE: protein
US-08-313-681A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-322-911-2
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1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
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100.0%; Score 535; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 8.2e-60;
Matches 101; Conservative 0; Mismatches 0; Indels (
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Faceur No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
FRIOM PEPLICATION NUMBER: 60/221,632
PRIOM APPLICATION NUMBER: 60/221,632
PRIOM APPLICATION NUMBER: 60/29,602
PRIOM APPLICATION NUMBER: 60/290,932
PRIOM FILING DATE: 2000-11-17
PRIOM FILING DATE: 2000-11-17
PRIOM FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: ABGUST 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION NUMBER: PCT/US93/06731
FILING DATE: September 27, 1994
ATTORNEY, AGASTY INFORMATION:
NAME: FALE, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKEY NUMBER: 35,136
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 aning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
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ORGANISM: Homo sapiens
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30 QALSYKGAVLRAVDGLNQRSSDENLYRLLELDPLPKGDKDSDTPKPVSFMVKETVCPRIM 89
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                                                                                     Query Match 68.0%; Score 364; DB 2; Length 156; Best Local Similarity 67.0%; Pred. No. 3.6e-38; Matches 67; Conservative 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                       61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
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Sequence 29, Application US/09917340

Sequence 29, Application US/09917340

GENERAL INFORMATION:

APPLICANT: Murphy, Christopher J.

APPLICANT: McAnulty, Jonathan F.

APPLICANT: McAnulty, Jonathan F.

APPLICANT: McAnulty, Jonathan F.

APPLICANT: McAnulty, Jonathan F.

TITLE OF INVENTION: Transplant Media

FILE REFERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: 60/221,632

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-11-17

PRIOR FILING DATE: 2001-05-15

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 29
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; ORGANISM: Equus asinus
US-09-917-340-35
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US-09-917-340-29
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                                                                    1 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                          0; Indels
                                                                                                                                                              61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKR 101
                                                                                                                                                                                      91 QOSPEDCDFKGGGLVKRCMGTVTLNQARGSFDISCDKDNKR 131
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Matches 101; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                             Sequence 33, Application US/09917340
Fatent No. 6696238
GENERAL INPORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE REPRENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
FRIOR FILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-17-29
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jergy 17, 1340-39
Sequence 35, Application US/09917340
Facent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
TILE REFERENCE: TPLANT-06468
CURRENT APPLICATION UNMERR: US/09/917,340
CURRENT FILING DATE: 2001-07-29
FRIOR APPLICATION NUMBER: 60/221,632
FRIOR APPLICATION NUMBER: 60/249,602
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2000-11-17
FRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENTING UNCE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SEGOID NOS: 96
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US-09-917-340-33
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US-09-917-340-35
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                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 159;
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 65.9%; Score 352.5; DB 2; Length Best Local Similarity 67.7%; Pred. No. 1.1e-36; Matches 65; Conservative 17; Mismatches 13; Indels
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MEDIUM TYRE: Floppy disk
MEDIUM TYRE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
ATTORNEY FAGENT INFORMATION:
NAME: MURSAHIGE KATE H.
REGISTRATION NUMBER: 20,959
REFERENCE/DOCKET NUMBER: 20,959
REFERENCE/DOCKET NUMBER: 20,959
RELEMONE: (202) 887-0763
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/08243879A; Sequence 34, Application US/08243879A; Patent No. 5708145; GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
ITILE OF INVENTION: A NEW PROFECTIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500; COUNTRY: USA
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PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Petentin Ver. 2.0
SEQ ID NO 34
LENGTH: 159
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MOLECULE TYPE: protein

US-08-243-879A-38
                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UGA

ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-UL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: MUMACHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 29,959
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1501
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CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 QOSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDK 97
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CORRESPONDENCE ADDRESS: ADDRESSES: PRINIE & EDMONDS LLP STREET: 1155 Avenue of the Americas CITY: New York STATE: New York STATE: New York
                                                  Sequence 4, Application US/08499523
Patent No. 5804558
GENERAL INPORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: FORRYAROV, VLADIMIR N.
ITILE OF INVENTION:
NUMBER OF SEQUENCES: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / MOLECULE TYPE: protein US-08-499-523-4
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RESULT 10
US-08-499-523-4
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30 QALSYREAVLRAVDRIANEQSSEANLYRILELDQPPKADBDPGTPKPVSFTVKETVCPRPT 89
         30 QALSYREAVLRAVDRLNEQSSEANLYRLLELDQPPKADEDPGTPKPVSFTVKETVCPRPT 89
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64.9%; Score 347; DB 1; Length 149;

Best Local Similarity 66.0%; Pred. No. 4.8e-36;

Matches 64; Conservative 17; Mismatches 16; Indels
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Sequence 40, Application US/08243879A

Sequence 40, Application US/08243879A

Patent No. 5708142

GENERAL INFORMATION:
APPLICANT: HARWIG, SILVA S.L.
TILLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE:
ATTER 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
                                                                                                                                                                                                                                                                                                                                               US-08-13-879A-36

| Sequence 36, Application US/08243879A |
| Sequence 36, Application US/08243879A |
| Patent No. 5708145 |
| GENERAL INFORMATION: |
| APPLICANT: LEHRER, ROBERT I. |
| APPLICANT: HARWIG, SYLVIA S.L. |
| TITLE OF INVENTION: A NEW PROTEGRIN |
| NUMBER OF SEQUENCES: 42 |
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: |
| APPLICANT: LEHRER |
| APPLICANT: LEHRER |
| CORRESPONDENCE ADDRESS: |
| ADDRESSE: MARLISON & FOERSTER |
| STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500 |
| CITY: Washington, DC |
| COUNTRY: USA |

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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION NUMBER: 23.0
ATTORNEY/AGENT INFORMATION:
NAME: MURACHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFRENCE/POCKET UNBER: 29,959
REFRENCE/POCKET UNBER: 2000-0540.22
TELECOMMULICATION INFORMATION:
TELECOMMULICATION 1870-1950
TELEFRAM: (202) 887-0763
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-243-879A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.9%; Score 347; DB 2; Length 147; Best Local Similarity 66.0%; Pred. No. 4.7e-36; Matches 64; Conservative 17; Mismatches 16; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/128,345

FILING DATE: 03-AUG-1998

CLASSIPICATION: 514

ATTORNEY FAGENT INFORMATION:

NAME: Coruzzi, Laura, A.

REGISTRATION NUMBER: 867-0054-999

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 869-9741

TELEXAK: (6141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 147 amino acide

TYPE: AM
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APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
APPLICANT: Gu, Chee L.
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah A.
APPLICANT: Lehrer, Robert I.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: ROKYGAKON, Vladimir N.
TITLE OF INVENTION: PROTECRINS
FILE REFERENCE: 8067-067-999
CURRENT APPLICATION NUMBER: US/09/385,328
CURRENT APPLICATION NUMBER: US 09/128,345
PRIOR APPLICATION NUMBER: US 09/128,345
PRIOR PILING DATE: 1998-08-03
PRIOR PILING DATE: 1998-08-03
PRIOR PILING DATE: 1996-10-28
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-385-328-4; Sequence 4, Application US/09385328; Patent No. 6653442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Sus scrofa
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64.94; Score 347; DB 1; Length 149;
Best Local Similarity 66.04; Pred. No. 4.8e-36;
Matches 64; Conservative 17; Mismatches 16; Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: ROBY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOSTWARE: Batentin Release #1.0, Version #1.25
SUSTWARE: PPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIPICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: MURSAHIGE, KATE H.
REGISTRATION NUMBER: 2000-0540.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-150
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-243-878A-42

i Sequence 42, Application US/08243879A

i Patent No. 5708145

GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

CTY: Washington, DC
COUNTRY: USA
ZIP: 2000 Fennsylvania Poc. N.W., Ste. 5500

CONPUTER: Floppy disk
COMPUTER: PIEM PC COMPATION
MEDIUM TYPE: Floppy disk
COMPUTER: PIEM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURSIFICATION NUMBER: US/08/43,879A
FILING SYSTEM: PC-DOS/MS-DOS
CUASSIFICATION NUMBER: US/08/243,879A
FILING AND ATE: NURABHER: Z30
ATTORNEY/AGENT INFORMATION:
NAME: NURABHER: Z30
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: Z30
ATTORNEY/AGENT INFORMATION:
TELERPHONE: CAOL OF THE HERERCOMMUTCATION INFORMATION:
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THE TELER
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 42:
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MOLECULE TYPE: protein

US-08-243-879A-40
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2, Appli 6, Appli 10, Appli 10, Appli 2, Appli 10, Appli 10, Appli 10, Appli 11, Appli 12, Appli 136, Appli

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Sequence 51, Application US/10603566

Publication No. US20040086966A1

Publication No. US20040086966A1

APPLICANT: Wittamer, Valerie

APPLICANT: Vandenbogaerde, Ann

APPLICANT: Detheux, Wichel

APPLICANT: Parmentier, Warc

TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 QVLSYKBAVLRAIDGINQRSSDANLYRLLDLDPPRPTMDGDPDTPKPVSFTVKETVCPRTT
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                                                                                                                                                                                        Sequence 51, P
Sequence 36, P
Sequence 28, A
Sequence 9, Ap
Sequence 28, A
                          Sequence 2, Ag
Sequence 6, Ag
Sequence 10, Ag
Sequence 2, Ag
Sequence 2, Ag
Sequence 8, Ag
Sequence 9, Ag
Sequence 10, Ag
Sequence 36, Ag
Sequence 36, Ag
Sequence 4
Sequence 2
Sequence 2
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 535; DB 3; Length 170; Best Local Similarity 100.0%; Pred. No. 1.2e-52; Matches 101; Conservative 0; Mismatches 0; Indels (
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US-09-539-443-6
US-09-539-443-10
US-10-627-829-2
US-10-627-829-8
US-10-627-829-10
US-10-627-829-10
US-10-637-829-10
US-10-344-709C-7
US-10-909-119-51
US-10-909-119-51
US-10-657-851-36
US-10-644-837-28
US-10-344-709C-28
                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/09917340
Patent No. US2002009369A1
GENERAL INPORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
TILE REFERENCE: TPLANT-06469
CURRENT APPLICATION UNDERS: US/09/917,340
CURRENT PILING DATE: 2000-07-29
FRIOR APPLICATION NUMBER: 60/221,632
FRIOR APPLICATION NUMBER: 60/249,602
FRIOR APPLICATION NUMBER: 60/249,602
FRIOR APPLICATION NUMBER: 60/249,602
FRIOR PILING DATE: 2000-01-17
FRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRGANISM: Homo sapiens US-09-917-340-32
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Sequence 4, Appl
Sequence 47, Appl
Sequence 32, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 1204, Appl
Sequence 33, Appl
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Sequence 51, App]
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535
1_QVLSYKEAVLRAIDGINQRS......VTLNQARGSFDISCDKDNKR 101
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Sequence 34,
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-603-566-51
US-10-344-709C-11
US-10-344-837-3
US-10-777-683-4
US-10-777-683-4
US-10-89-485-51
US-10-87-485-51
US-10-87-485-51
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US-10-89-485-51
US-10-89-485-51
US-10-89-4837-33
US-10-87-4817-35
US-10-657-851-35
US-10-657-851-35
US-10-657-851-35
US-10-657-851-35
US-10-657-851-35
US-10-657-851-39
US-10-844-837-29
US-10-844-837-29
US-10-844-837-34
US-10-844-837-34
US-10-657-851-39
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Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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Maximum DB E
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Sequence 47, Application US/10909119
Publication No. US20050079578A1
GENERAL INFORMATION:
APPLICANT: Centanni, John M.
APPLICANT: Allen-Hoffmann, Lynn
TITLE OF INVENTION: Human Skin Equivalente Expressing Exogenous Polypeptides
FILE REFERENCE: STRATA-09123
CURRENT APPLICATION NUMBER: US/10/909,119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 QVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Richard B. Moss
APPLICANT: Richard B. Moss
APPLICANT: Akitoshi Ishizaka
APPLICANT: Teruo Kirikae
TITLE OF INVENTION: Method for Assessment of Cystic Lung Fibrosis
FILE REPERENCE: 074236
CURRENT APPLICATION NUMBER: US/10/777,683
CURRENT FILING DATE: 2004-02-13
PRIOR PILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 535; DB 5;
100.0%; Pred. No. 1.2e-52;
tive 0; Mismatches 0;
                  APPLICANT: Homan, Jane
APPLICANT: Bremel, Kobert D.
TITLE OF INVENTION: Targeted Biocides
FILE REFERENCE: IOGEN-09014
CURRENT APPLICATION NUMBER: US/10/844,837
CURRENT FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn version 3.2
SEQ ID NO ED ID NOS: 101
LENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/1077683 Publication No. US20050032117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100. Matches 101; Conservative
APPLICANT: Imboden, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100. Matches 101; Conservative
                                                                                                                                                                                                                                                                                 TYPE: PRT
CORGANISM: Homo sapiens
US-10-844-837-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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Sequence 11, Application US/10344709C

PUBLication No. US20040170642A1

GENERAL INFORMATION:

APPLICANT: JORG FRITZ ET AL.

TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: APPLICATION WHORER: 2003-02-14

PRIOR PRILING DATE: 2003-02-14

PRIOR PELING DATE: 2001-08-17

PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 11

LENGTH: 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide US-10-344-709C-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 QVLSYKRAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPRPVSFTVKETVCPRTT 90
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100.0%; Score 535; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 170;
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100.0%; Pred. No. 1.2e-52;
tive 0; Mismatches 0;
                CURRENT APPLICATION NUMBER: US/10/603,566
CURRENT FILING DATE: 2003-06-25
PRIOR PLILING DATE: 2001-07-09
PRIOR PLING DATE: 2001-07-09
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 51
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; Sequence 32, Application US/10844837
; Publication No. US20050014932A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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FILE REFERENCE: 9409/2212
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-287-436A-1204
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                                                                                                                                  Query Match
100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                    Sequence 51, Application US/10893485
Publication No. US20050155090A1
GENERAL INFORMATION:
APPLICANT: Wittemer, Valerie
APPLICANT: Communi, David
APPLICANT: Vandehogaerde, Ann
APPLICANT: Detheux, Michel
APPLICANT: Parmentier, Marc
CURRENT FILING DATE: 2004-07-30 NUMBER OF SEQ ID NOS: 128 SOFTWARE: Patentin version 3.2 SEQ ID NO 47 LENGTH: 170
                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-119-47
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; ORGANISM: Homo sapiens
US-10-657-851-32
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Best Local Similarity
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TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR FILE REFERENCE: 9409/2045C
CURRENT APPLICATION NUMBER: US/10/893,485
CURRENT PILING DATE: 2004-07-16
PRIOR PLICATION NUMBER: US 60/303,858
PRIOR FILING DATE: 2001-07-09
PRIOR PLICATION NUMBER: US 09/905,253
PRIOR PLING DATE: 2003-06-25
PRIOR PLING DATE: 2003-06-25
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-07-13
PRIOR PLING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 97
SEQ ID NO 5: 97
LENGTH: 170
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100.0%; Score 535; DB 5; Length 170;
Best Local Similarity 100.0%; Pred. No. 1.2e-52;
Matches 101; Conservative 0; Mismatches 0; Indels
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; Publication No. US20050202421A1
; GENERAL INFORMATION
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Homo sapiens
US-10-893-485-51
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ORGANISM: Homo sapiens
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TYPE: PRT
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TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: RHEUMATOID ARTHRITIS FILE REFERENCE: 10872.514012 AND TREATMENT OF TILE REFERENCE: 10872.514012 AND TREATMENT OF THE REPRENCE: 2002-10-31 PRIOR PELLING DATE: 2002-10-31 NUMBER OF SEQ ID NOS: 1446 SEQ ID NOS: 1446 SEQ ID NO 1204

LENGTH: 170
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Fatent No. US20020090369A1
GERREAL INFORMATION!
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
ITILE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT FILING DATE: 2001-07-29
FRIOR PILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,602
FRIOR FILING DATE: 2000-11-17
PRIOR PILING DATE: 2001-05-15
FRIOR FILING DATE: 2001-05-15
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US-09-917-340-33
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-09-917-340-33
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US-10-844-837-33
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Sequence 33, Application US/10844837 Publication No. US20050014932A1 GENERAL INFORMATION: APPLICANT: Imboden, Michael

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GENERAL INFORMATION:
APPLICANT: Centanni, John M.
APPLICANT: Allen-Hoffmann, Lynn
TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
FILE REFERENCE: STRATA-09123
CURRENT APPLICATION NUMBER: US/10/909,119
CURRENT FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.2
SEQ ID NO 48
LENGTH: 170
TYPE: PRT
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APPLICANT: Homan, Jane
APPLICANT: Bremel, Robert D.
TITLE OF INVENTION: Targeted Biocides
FILE REFERENCE: IOGEN-09014
FILE REFERENCE: 10GEN-09014
CURRENT APPLICATION NUMBER: US/10/844,837
CURRENT FILING DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 101
SOFTMARE: PatentIn version 3.2
SEROID NO 33
LENGTH: 170
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Publication No. US20050089836A1
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Reid, Ted W.
TILLE OF INVENTION: Transplant Media
FILLE REFERENCE: TPLANT-06468
CURRENT FILLION DAPPLICATION NUMBER: US/10/657,851
CURRENT FILLION DATE: 2001-09-09
FRIOR APPLICATION NUMBER: US/09/917,340
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; Sequence 48, Application US/10909119
; Publication No. US20050079578A1
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Best Local Similarity 68.0%
Matches 68; Conservative
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US-10-844-837-33
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US-10-909-119-48
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1 OVLSYKBAVLRAIDGINORSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
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JOS-09-91. Application US/09917340

GENERAL INPORMATION:
JAPPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
TILE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: 60/29/917,340

CURRENT PILING DATE: 2001-07-29

PRIOR APPLICATION NUMBER: 60/249,602

PRIOR FILING DATE: 2000-11-17

PRIOR FILING DATE: 2000-11-17

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 96

SOFTWARE: Patentin Ver. 2.0

SEGIO ID NO 35

LENGTH: 156
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2000-11-17
PRIOR PILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
LENGTH: 170
                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Equus caballus
US-10-657-851-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Equue asinue
US-09-917-340-35
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 68; Conservat
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US-09-917-340-35
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Search completed: January 12, 2006, 21:54:02 Job time : 41.7417 secs

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Sequence 1068, Applequence 905, Applequence 296, Applequence 37, Applequence 37, Applequence 34, Applequence 187, Applequence 188, Applequence 188, Applequence 176, Applequence 176, Applequence 27, Applequence 27, Applequence 27, Applequence 1186, Applequence 27, Applequence 27, Applequence 27, Applequence 27, Applequence 37, Appleq

Perfect score:

Sequence:

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APPLICANT Tangy Y Tom
APPLICANT Tangy Y Tom
APPLICANT Chenghua
APPLICANT Chen, Rui-hong
APPLICANT Cao, Yi-Cheng
APPLICANTON NOWERR: US/11/000,463
CURRENT APPLICATION NUMBER: US/21,265
PRIOR APPLICATION NUMBER: D0/291,265
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2001-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PILING DATE: 2000-01-7
PRIOR APPLICATION NUMBER: 09/611,746
PRIOR APPLICATION NUMBER: 09/611,746
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR PILING DATE: 2000-09-15
US-10-615-668-5
US-11-118-472-1068
US-11-113-47-905
US-10-467-657-2966
US-11-126-313-37
US-11-126-313-37
US-11-055-877-34
US-10-055-877-189
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US-11-055-877-189
US-11-052-554A-176
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 347, Application US/11000463
Publication No. US20050266423A1
GENERAL INFORMATION:
      ; ORGANISM: Homo sapiens
US-11-000-463-347
   SEQ ID NO 347
LENGTH: 1061
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Sequence 348, App
Sequence 47, Appl
Sequence 3750, Ap
Sequence 68, Appl
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55, Appl
56, Appl
35, Appl
36, Appl
37, Appl
2964, Ap
878, Appl
878, Appl
878, Appl
878, Appl
878, Appl
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535
1 QVLSYKBAVLRAIDGINQRS......VTLNQARGSFDISCDKDNKR 101
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Sequence 4
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1: /cgnZ 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

2: /cgnZ 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*

3: /cgnZ 6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

4: /cgnZ 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

5: /cgnZ 6/ptodata/1/pubpaa/USO9 NEW PUB.pep:*

6: /cgnZ 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*

7: /cgnZ 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*

8: /cgnZ 6/ptodata/1/pubpaa/USO1 NEW PUB.pep:*
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Copyright (c) 1993 - 2006 Compugen Ltd
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US-11.067-295-42

US-11.100-183-15

US-11.137-465-35

US-11.137-465-35

US-11.137-465-36

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US-11.137-465-36

US-11.138-487-37

US-11.0995-561-876

US-11.095-561-877

US-11.095-561-877

US-11.052-554A-43

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Match
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22 DANLYRLLDLDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPED-----CDFKKDGLVK 76

8

43, Appl 39, Appl 1536, Ap 40, Appl 48, Appl 190, Appl

Sequence Sequence Sequence

Score

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Result

Sequence Sequence

US-11-135-855-40 US-11-174-150-48 US-10-055-877-190

Query Match 11.4%; Score 61; DB 7; Length 1061; Best Local Similarity 26.8%; Pred. No. 20; Matches 22; Conservative 11; Mismatches 21; Indels

28; Gaps

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6 KEAVLRAIDGINQRSSDANLYRLL----DLDPRPTMDGDPDTPKPVSFTVKETVCPRTT 60
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11.1%; Score 59.5; DB 6; Length 389;
Best Local Similarity 26.8%; Pred. No. 8.6;
Matches 22; Conservative 10; Mismatches 31; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3750, Application US/10467657
; Publication No. US20050260581A1
general information.
; GERREAL information:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
APPLICANT: FONTANA Maria Rita
; APPLICANT: POSTZA Mariagrazia
; APPLICANT: MASIGNANI vega
; APPLICANT: MASIGNANI vega
; APPLICANT: MONACI Elisabetta
; TITLE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; RIOR APPLICATION NUMBER: US/10/467,657
; RIOR APPLICATION NUMBER: 2001-02-12
; RIOR APPLICATION NUMBER: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3750
; LENGTH: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
11.2%; Score 60; DB 7; Length 349;
Best Local Similarity 28.4%; Pred. No. 6.5;
Matches 19; Conservative 6; Mismatches 30; Indels
                      CURRENT FILING DATE: 2005-06-07
CURRENT FILING DATE: 2005-06-07
PRIOR PILING DATE: 2005-06-07
PRIOR FILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-03-05
PRIOR PLING DATE: 2001-03-05
PRIOR PLING DATE: 2001-03-05
PRIOR PLING DATE: 2000-03-06
PRIOR PLING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-03-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-47
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---SGTIK----VKATQKKANDGEWYHVDIQRDGR-- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, Kila-Bong
APPLICANT: Qian, Xiaohong B.
APPLICANT: Wehrman, Yaohong B.
APPLICANT: Wehrman, Tom
APPLICANT: Zhau, Piwei
APPLICANT: Zhau, Ping
APPLICANT: Zhau, Ping
APPLICANT: Zhau, Ping
APPLICANT: Cao, Yi-Cheng
APPLICANT: Drmanac. 18doje T.
TITLE OF INVENTION: NOVEL: 2004-11-29
PRIOR APPLICATION NUMBER: US/11/000,463
CURRENT APPLICATION NUMBER: DCY/US01/02623
PRIOR PILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR PILING DATE: 2000-07-17
PRIOR PILING DATE: 2000-07-17
PRIOR PPLING DATE: 2000-09-05
PRIOR PLING DATE: 2000-09-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 --SGTISVNSRRTPFTASGESE 199
                                                                                                                                        180 --SGTISVNSRRTPFTASGESE 199
                                                                                                                                                                                                                                                                                                               Sequence 348, Application US/11000463 Publication No. US20050266423A1 GENERAL INFORMATION:
                                                                      77 RCMGTVTLNQARGSFDISCDKD 98
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tang, Y Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Rui-hong
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ORGANISM: Homo sapiens
141 DGNLYLLLDMG-
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352 QRSVMYRCRNCHPKSQVPFWHC 373

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; OTHER INFORMATION: Ceres Seq. ID no. 6425770 US-10-667-295-43
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7
             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Mascia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REPERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: PastSRQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59.5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Corynebacterium glutamicum
US-11-055-822-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-667-295-43

Sequence 43. Application US/10667295
Publication No. US2050257293A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cn 11.1%;
1 Similarity 32.1%;
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
LOCATION: (1)...(102)
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Best Local Similarity
           -11-055-822-68
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US-11-100-183-15
US-11-100-183-15
Sequence 15, Application US/11100183
Sequence 15, Application No. US20050272074A1
GENERAL INFORMATION:
APPLICANT: Stratageme California
TITLE OF INVENTION: Compositions And Methods For Reverse Transcription
CURRENT APPLICATION NUMBER: US/11/100,183
CURRENT FILING DATE: 2004-04-06
PRIOR APPLICATION NUMBER: US 6/559,810
PRIOR PELING DATE: 2004-04-06
NUMBER OF SEQ ID NOS: 61
SOTWARE: Patentin version 3.2
SEQ ID NO 15
LENGTH: 236
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                                                                                                                                               35 SVVGAVDGVB-----TNSNSEDK 62
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                                                                                                              8 AVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDC
                                                           32; Gaps
                                                        24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 10.8%; Score 58; DB 6; Length 141; 1 Similarity 23.3%; Pred. No. 3.6; 20; Conservative 10; Mismatches 24; Indels
Query Match
10.8%; Score 58; DB 6; Length 102;
Best Local Similarity 23.3%; Pred. No. 2.4;
Matches 20; Conservative 10; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM FILE REFERENCE: 11696-047001
FILE REFERENCE: 11696-047001
CURRENT PELLON NUMBER: US/10/667,295
CURRENT FILING DATE: 2003-09-17
PRIOR FILING DATE: 2002-09-17
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(141)
; OTHER INFORMATION: Ceres Seq. ID no. 6425769
US-10-667-295-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 SEKDKGKRKLCVGSQALNYRRDHMEI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 DPKKDGLVKRCMGTVTLNQARGSFDI 93
                                                                                                                                                                                                                      68 DPKKDGLVKRCMGTVTLNOARGSFDI 93
                                                                                                                                                                                                                                                                            63 SEKDKGKRKLCVGSQALNYRRDHMEI 88
                                                                                                                                                                                                                                                                                                                                                                                       US-10-667-295-42
; Sequence 42, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
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; ORGANISM: Pasteurella multocida
US-11-100-183-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
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US-11-137-465-36
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SEQ ID NO 36
LENGTH: 993
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                                                                                                                                                                                                                                                    US-11-137-465-35
                                                                                                                                                                                  LENGTH: 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                            12 AIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFT----VKETVCPRTTQQSPE-- 65
                                                                                                                                                                              66 ------RGSPDIS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Acentin Ver. 2.1
SED ID NO 566
LENGTH: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 DGING--RSSDANLYRLLDLDPRPTM----DGDPD---TPKPVSFTVKETVCPRTTQQ-- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 NGVFQLINTSILNAFGLNDKONRGEEMSHYYDEQPDVKSNPKRISYQIKNAQLELTTDAGV 77
                                                47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.7%; Score 57; DB 6; Length 244;
Best Local Similarity 25.5%; Pred. No. 9.5;
Matches 24; Conservative 15; Mismatches 43; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence
10.7%; Score 57.5; DB 7; Length 236; 23.8%; Pred. No. 7.9; tive 14; Mismatches 38; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 FSKDNVDFGSDLLIKTFLKEHPPGPSKTIADVGC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 -SPEDCDFKKDGLVKRCMGTVTLNQARGSFDISC 95
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CURRENT PILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US/10/239,663
PRIOR FILING DATE: 2002-09-24
PRIOR PLING DATE: 2001-09-24
PRIOR PLING DATE: 2001-03-22
PRIOR PLING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/192,158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/11137465
Publication No. US2005025558A1
GENERAL INFORMATION:
APPLICANT: Murdoch, Paul R.
APPLICANT: Marai, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Gablick, Karen
TITLE OF INVERTION: NOVEL COMPOUNDS
FILE REFERENCE: GPS0018
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 566, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                            31; Conservative
                                                                                                                                                                                                                                                                      95 CDK---DNKR 101
                                                                                                                                                                                                                                                                                                                  143 CORLGIDNSK 152
                    Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                        US-10-793-626-566
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 PVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270 PVGFMLQP---DRKTCKDIDECRLANGGCDHICRNTV-----GSFECSCKKGYK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 PVSPTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNK 100
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; Publication No. US20850260713A1
; GENERAL INFORMATION:
APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REPERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
                                                                                                                                                                                                                                                                                                                                                                                DB 7; Length 897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 7; Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.6%; Score 56.5; DB 7; Length 99; 30.9%; Pred. No. 64; tive 6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                Score 56.5; DB 7; Length 8
Pred. No. 56;
6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Murdoch, Paul R.
APPLICANT: Mixti, Safia, K.
APPLICANT: Smith, Randall, F.
APPLICANT: Smith, Randall, F.
APPLICANT: Stang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Xiang, Zhaoying
APPLICANT: Kabnick, Karen
APPLICANT: Wabnick, Karen
APPLICATION: WOWEL COMPOUNDS
FILE REFERENCE: GP50018
CURRENT APPLICATION NUMBER: US/11/137,465
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: PC7/US01/09226
PRIOR FILING DATE: 2001-03-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/192,668
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: 60/200,166
PRIOR PILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36, Application US/11137465
Publication No. US20050255558A1
GENERAL INPORMATION:
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Best Local Similarity 30.9%;
Matches 17; Conservative
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Best Local Similarity 30.94
Matches 17; Conservative
                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-11-137-465-36
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ORGANISM: Artificial Sequence FEATURE:
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 34.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-995-561-878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-995-561-878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 PVSPTVKETVCPRITQQSPEDCDPKKDGLVKRCMCTVTLNQARGSFDISCDKDNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 PIGFTLQ---VDGKTCKDIDECQTRNGGCNHPCKNTV-----GSPDCSCKKGFK 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%; Score 56.5; DB 7; Length 997; 30.9%; Pred. No. 64; tive 6; Mismatches 23; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 7834, Application US/10467657
; Publication No. US20050260581A1
GENERAL INFORMATION:
    APPLICANT: CHIRON Spa
    APPLICANT: PONTANA Maria Rita
    APPLICANT: PONTANA Maria Raia
    APPLICANT: PONTANA Maria Raia
    APPLICANT: PONTANA Maria Raia
    APPLICANT: MONACI Elisabetta
    TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
    FILE REFERENCE:
    CURRENT PILLING DATE: 2003-08-11
    PRIOR APPLICATION NUMBER: GB-0103424.8
    PRIOR PLLING DATE: 2001-02-12
    NUMBER OF SEQ ID NOS: 9218
    SOFTWARE: SeqWin99, version 1.04
    SEQ ID NO 7834
    TONGY 1334
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CURRENT FILING DATE: 2005-04-21

PRIOR APPLICATION NUMBER: 60/256,704

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

PRIOR PILING DATE: 2000-12-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-10

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-08-29

PRIOR PLING DATE: 2001-07-24

PRIOR PLING DATE: 2001-07-24

PRIOR PLING DATE: 2001-09-14

PRIOR PLING DATE: 2001-09-14

PRIOR PLING DATE: 2001-09-14

PRIOR PLING DATE: 2001-05-29

PRIOR PLING DATE: 2001-05-02

NUMBER OF SEQ ID NOS: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 30.9
Matches 17, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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US-10-467-657-7834
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Sequence 878, Application US/10995561
Publication No. US2005272054A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REFERENCE: CLOOL559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SEQ ID NO 878
LENGTH: 729
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Sequence 2964, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION, WILLIAM JOHN
APPLICANT; KIRMERLY,
ITILE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILLE REPERENCE: 190486002
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PELICATION NUMBER: 60/164,258
PRIOR PLILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SEQ ID NO 2964
LENGTH: 5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VLSYKBAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPDTPKPVSFTVKETVC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: January 12, 2006, 21:54:25
Job time : 4.47232 secs
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; OTHER INFORMATION: variable amino acid
US-10-793-626-2964
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GenCore version 5.1.6 Copyright (c) 1993 - 2006 Compugen Ltd.	25 24 28	451 442.5 433.5 432	51.3 50.3 49.3	156 176 173 159	
OM protein - protein search, using sw model	30	432 431.5	49.1	159 173	
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	33	427.5	48.6	155	u
826.886 Million cell updates/sec	34	424.5	48.3	149	"
	35	421.5	48.0	172	
le: US-10-815-562-2	36	418.5	47.6	147	••
Perfect score: 879	37	418.5	47.6	149	w
Sequence: 1 MKTQRDGHSLGRWSLVLLLLKRIVQRIKOFLRNLVPRTES 170	38	418.5	47.6	149	•••
	39	418.5	47.6	149	••
Scoring table: BLOSUM62	40	418.5	47.6	149	CA
Gapop 10.0 , Gapext 0.5	41	415.5	47.3	147	œ
	42	415.5	47.3	149	w
Searched: 2443163 segs, 439378781 residues	43	415.5	47.3	149	æ
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Adx08377 Myeloid c
Adz80368 Human CRA
Adz80365 Human CRA
Adx08376 BNAP-28 m
Abb07701 Murine ca
Abb07704 Bovine pe
Aau90993 Transplan
Adx08371 Bacceneci
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Adx18157 Antimicro
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Aaw18159 Antimicro
Aaw18159 Antimicro
Adx18362 Pig prote
Ad118362 Pig prote
Ad118368 Pig prote

ALIGNMENTS

Human; cationic protein; lipopolysaccharide binding; anticoagulant; CAP18; reactive nitrogen inhibitory protein; RNIP; gram negative sepsis; coagulation-related disorder; disseminated intravascular coagulation. A human cationic protein designated CAP18. AAB07901 standard; protein; 170 AA 14-NOV-2000 (first entry) AAB07901; RESULT 1

sapiens Homo

Location/Qualifiers 134. .170 /note= "reactive nitrogen inhibitory protein" Protein Key

US6103888-A.

92US-00916761. 92US-00916765. 93WO-US006731. 99US-00322911. 94US-00313681 96US-00691280 17-JUL-1992; 17-JUL-1992; 15-JUL-1993; 01-JUN-1999; 27-SEP-1994; 01-AUG-1996; 15-AUG-2000

Ξ Hirata (PANO-) PANORAMA RES INC Larrick JW, Wright SC,

WPI; 2000-531989/48. N-PSDB; AAA59574.

Novel human cDNA encoding cationic proteins having lipopolysaccharide binding and anticoagulant activity, useful for treating and diagnosing gram negative sepsis and disseminated intravascular coagulation.

Disclosure; Col 29-30; 46pp; English.

The present sequence represents a human cationic protein, having lipopolysaccharide binding and anticoagulant activity. The polypeptide is

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A_Geneseq_21:*

length: 0 length: 2000000000

DB seq] DB seq]

Minimum I Maximum I

genesequ1980s:* genesequ2000s:* genesequ2000s:* genesequ2001s:* genesequ2003s:* genesequ2003s:* genesequ2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SUMMARIES	
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No.	Score	Match	Watch Length DB	DB	ΩI	Description
	879	100.0	170	9	AAB07901	Aab07901 A human c
7	879	100.0	170	-	ADF18219	Adf18219 Protein 8
e	879	100.0	170	œ	ADI29582	Adi29582 Human CAP
4	879	100.0	170	8	ADJ82973	Adj82973 Human Pep
S	879	100.0	170	8	ADR47315	
y	879	100.0	170	σ	ADW43827	Adw43827 Mouse che
7	875	99.5	169	æ	ADK70797	Adk70797 Human CAP
60	874	99.4	170	~	AAR92924	Aar92924 Prepro-FA
σ	874	99.4	170	'n	AAU90996	Aau90996 Transplan
10	874	99.4	170	7	ADP65263	Adp65263 Human cat
11	874	99.4	170	œ	ADN41827	Adn41827 Human LL-
12	874	99.4	170	æ	ABM80449	Abm80449 Tumour-as
13	874	99.4	170	σ	ADX08374	Adx08374 Cathelici
14	874	99.4	170	0	ADZ80363	Adz80363 Human cat
15	865	98.4	170	S	ABB07707	Abb07707 Human pep
16	819	93.2	177	4	AAU31061	Novel
17	761	86.6	152	m	AAG03781	Aag03781 Human sec
18	730	83.0	140	æ	ADJ82974	Adj82974 Human Pep
19	069	78.5	170	σ	AEA00315	Aea00315 Human cat
20	493.5	56.1	172	6	ADZ80366	
21	468.5	53.3	171	Ŋ	ABB07703	Abb07703 Rabbit pe
22	457.5	52.0	170	Ŋ	AAU90997	-
23	457.5	52.0	170	σ	ADX08375	Adx08375 Myeloid c
24	451	51.3	156	Ŋ	AAU90999	Aau90999 Transplan

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designated CAP18. Amino acids 134-170 of CAP18 represent a reactive nitrogen inhibitory protein (RNIP). The CAP18 polymucleotide is useful for producing cationic proteins. The CAP18 polypeptide is useful for treating and diagnosing lipopolysaccharide-associated conditions such gram negative sepais, and/or coagulation-related disorders, such as disseminated intravascular coagulation
              useful
                                                                                                                                                                                                  MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                       atch 170; Score 879; DB 3; Length 170; cal Similarity 100.0%; Pred. No. 4e-89; 170; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                      ADF18219 standard; protein; 170
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KOCZULLA A R.
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                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein sequence.
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                                                                                               Sequence 170 AA;
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The present invention is based on the finding that human antimicrobial peptide Li-37 APS18218 is capable of inducing functionally important anglogenesis in cell culture and in vivo by activation of the receptor molecule FPRL1. LL-37 can be used in the preparation of a pharmaceutical

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                                                                                                                                                                                                                                                                                                                                                                                                  LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
             resulting in, a reduced level of angiogenesis or arteriogenesis, or for the treatment of (infected) wounds or cancer. The disease may be associated with reduced blood flow, such as atherosclerosis, coronary heart disease, stroke, arterial occlusive disease or an ulcer. Suppression of angiogenesis through inhibition of IL-37 can be used to treat tumours, especially a carcinoma or sarcoma including cancer of the bile duct, brain, breast, colon, stomach, male and female reproductive organs, lung and airways, skin, gallbladder, liver, nasopharynx, nerve cells, kidney, prostate, and Kaposi's sarcoma (all claimed). The present protein sequence is not explained in the specification.
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or
for
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composition for the prevention or treatment of a disease caused by,
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                                                                                                                                                                                                                                                  100.0%; Score 879; DB 7; Length 170;
100.0%; Pred. No. 4e-89;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI29582 standard; protein; 170
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Best Local Similarity 100.0%;
Matches 170; Conservative 0
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14-MAR-2003; 2003JP-00070932.
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                                                                                                                                                                                                                     Sequence 170 AA;
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of bacteria
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WPI; 2004-099371/10.
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                                                                                                         LDPRPTMDGDPDTPKPVSFTVKBTVCPRTTQQSPEDCDPKKDGLVKRCMGTVTLNQARGS 120
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diseases, ARDS and bronchial asthma. The present sequence is human
                                                                        1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                                                   MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                         Gaps
                                                                                                                                                                                                                                                                 pep714-related peptide; precursor; human; secreted peptide; Pep714; oral mucositis; oral lesion; cystic fibrosis; respiratory infection; pneumonia.
                                                                                                                                        PDISCDYDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
                                                                                                                                                  PDISCONDINKRPALLGOPFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
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0
                                      100.0%; Score 879; DB 8; Length 170; 100.0%; Pred. No. 4e-89; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   /note= "dibasic peptidase cleavage site"
130. .131
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/note= "dibasic peptidase cleavage site"
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                                                                                                                                                                                                                                                                                                                                                                                                                   label= antibacterial_protein_FALL-39
34. 170
label= antibacterial_protein_LL-37
                                                                                                                                                                                                                                                   Human Pep714-related peptide precursor SEQ ID NO: 1.
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note= "dibasic peptidase cleavage
51. .152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Niknejad A;

    .30
    /label= signal_peptide
    .131
    /label= propeptide

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2003US-0438602P.
                                                                                                                                                                                                                                   (first entry)
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                                                Best Local Similarity 100.
Matches 170; Conservative
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                        Sequence 170 AA;
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ADJ82973
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Novel Pep714-related polypeptide having biological activity, useful for treatment and prevention of microbial or viral infection, cystic fibrosis and chronic respiratory infections.
                                                                                                                                                                                                    The present invention relates to a Pep714-related peptide. This is useful for inhibiting microbial propagation, preferably viral propagation, and in the treatment of chemocherapy and radiotherapy induced oral mucositis, oral lesion, ventilator associatementia, chronic respiratory infections and cystic fibrosis. The present sequence is a Pep714-related peptide precursor protein shown in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cystic pulmonary fibrosis; cationic antimicrobial protein; CAP18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 879; DB 8; Length 170;
100.0%; Pred. No. 4e-89;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDISCDKDNKRFALLGDFFRKSKEKIGKBFKRIVQRIKDFLRNLVPRTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cationic antimicrobial protein-18
                                                                                                                                          Disclosure; Page 91-92; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR47315 standard; protein; 170 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2003; 2003US-0447310P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 170; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-629858/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 170 AA;
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Example 2; SEQ ID NO 51; 183pp; English.

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evaluating cystic pulmonary fibrosis by associating comparison of obtained results. The invention further comprises: a kit for carrying out the evaluating method, comprising a solid-phase component and an antibody coupled with an antigenic peptide having a sequence of ADRA7112, or a solid-phase component comprising an immobilised antibody (first antibody solid-phase component comprising an immobilised antibody (first antibody) useful for evaluating cystic peptide, and the method or kit are useful for evaluating cystic pulmonary fibrosis in an individual, where the evaluation includes diagnosis for the presence or absence of a risk of cystic pulmonary fibrosis, evaluation of serious or acute conditions, or the evaluation of the advanced grade of the disease. The method enables simple, cost-effective, rapid, highly sensitive and highly accurate evaluation of the actions conditions, or the advancement of the pulmonary diseases. This sequence represents the human advancement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAP18 protein of the invention.
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Sequence 170 AA;

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LDPRPTWDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                       LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                         1 MKTQRDGHSLGRWSLVLLLLGLVWPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                    1 MKTQRDGHSLGRWSLVLLLLCLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                      Gape
                                                                                                                                                                                                                                              PDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
                                                                                                                                                                                                                          121 FDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
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                   Score 879; DB 8; Length 170;
Pred. No. 4e-89;
                                                   Indels
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100.0%; Scolution 100.0%; Pred. No. %colution 0; Mismatches
                   Query Match 100.
Best Local Similarity 100.
Matches 170; Conservative
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Mouse chemerin peptide SEQ ID NO 51. ADW43827 standard; peptide; 170 AA (first entry) 24-MAR-2005

neurological disease; hyperproliferative disorders; cytostatic; chemerin. İymphoproliferative disease; dermatological disease; dermatological; hemostatic; inflammation; antiinflammatory; hematological disease; immune disorder; neoplasm; cardiovascular-gen.; cns-gen.; gene therapy; diagnosis; cell signaling; gene therapy;

Mus musculus

WO2005000875-A2.

06-JAN-2005.

25-JUN-2003; 2003US-00603566.

25-JUN-2004; 2004WO-EP006945.

(EURO-) EUROSCREEN SA.

Ooms FDR;

WPI, 2005-058121/06.

Communi D,

Wittamer V,

Detheux M, Parmentier M, Loison C;

New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, Gaucher's Disease, or histiocytosis.

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The invention describes a polypeptide (1) of up to 50 amino acids where the polypeptide binds specifically to a chemerink polypeptide. Also described are: a mucleic acid sequence encoding (1); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (1) and an isolated chemerink polypeptide or a nucleic acid sequence of (1); an antibody that selectively binds to (1); identifying an agent that modulates the interaction between a chemerin polypeptide and a gent that modulates the interaction between a chemerin polypeptide and a gent that modulates the interaction between a chemerink polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a Chemerink polypeptide is detecting the presence, in a sample, of an agent that modulates the function of Chemerink polypeptide; detecting the presence, in a sample, of an agent that modulates the function of Chemerink Polypeptide is disorder characterized by dysregulation of Chemerink (polypeptide) signaling; a kit, for screening agents that modulate the signaling activity of Chemerink Polypeptide signaling, a kit, for screening agents that chemerink polypeptide signaling, a kit, for screening activity of Chemerink Polypeptide signaling activity of chemerink Polypeptide signaling activity of chemerink polypeptide signaling activity of chemering polymeric or composition or activity of chemering polymeric or activity of therapeutic) composition or expression vector is useful for preparing a matchody inhibiting call proliferation. The chemering a disease, and any other chemering a disease, and any other chemedicament for a unihibiting call proliferation, where the medicament is changed by supputed signal and second or inhibiting call proliferation, where the medicament is changed signal disease, and solve or confidence or medicament for activity of diseases, histiocytosis, and any other hyperproliferative disease. The polyp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  processing of immature chemerin.
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61 LDPRPTWDGDPDTPKPVSPTVKBTVCPRTTQQSPEDCDFKKDGLVKRCWGTVTLNQARGS
                                                                                                                                   PDISCDKDNKRFALLGDFPRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES
                                                                                             121 FDISCOKDNKRFALLGDFFRKSKEKIGKEFKRIVORIKDFLRNLVPRTES
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121

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ADK70797 standard; protein; 169 AA. 06-MAY-2004 (first entry)

alpha-helix; thionine; antibacterial; antifungal; plant; fungi resistance; rice blast fungus; Ceratocystis fimbriata; bacteria; Pseudomonas; antimicrobial; rabbit; CAP18.

Human CAP18 full-length protein.

Ното варіеля

JP2003204794-A.

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WPI; 2002-268995/31
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                            (BOMA/) BOMAN
                                             Agerberth B,
         13-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-FEB-2002.
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                                                                                                                                                                                               cytotoxic
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                                                                                           Novel
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                                                                                                                                                       The invention relates to a novel polypeptide composition for preventing disease in an organism which comprises one or more types of polypeptide which have an alpha-helix structure and/or thionine component. The composition of the invention demonstrates antibacterial and antifungal activities and may be useful for preventing a disease in an organism, for generating cultivated plants and in providing resistance to plant tissue against fungl such as Pyricularia oryzae (rice blast fungus), Ceratocystis finbriata and bacteria such as Pseudomonas etc. The composition has high antimicrobial activity at low concentration. The current sequence is that of the rabbit CAP18 full-length protein of the
                                                                                                  Antimicrobial polypeptide composition for a plant pathogen, comprises one or more types of thionine and/or a polypeptide having an alpha helix structure, as an active ingredient.
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                                                                                                                                                                                                                                                                                                                             LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS
                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      PDISCDKONKRPALLGDPPRKSKEKIGKBPKRIVQRIKDPLRNIVPRTB 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FALL-39; cathelin; antibiotic; antimicrobial; antibacterial.
                                                                                                                                                                                                                                                                                           Length 169;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                         / Match 99.5%; Score 875; DB 8; L. Local Similarity 100.0%; Pred. No. 1.1e-88; les 169; Conservative 0; Mismatches 0;
                                                                                                                                        Disclosure; SEQ ID NO 38; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .131
/label= Prepro-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR92924 standard; protein; 170 AA
                                                               (TOYW ) TOYOTA CHUO KENKYUSHO
                           15-JAN-2002; 2002JP-0006607.
                                            15-JAN-2002; 2002JP-0006607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95WO-SE001030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                 WPI; 2004-102620/11
                                                                                                                                                                                                                                                                       Sequence 169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prepro-FALL-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9608508-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
         22-JUL-2003
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                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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Novel cathelin-like prepro-FALL-39 (AAR92924) is the precursor of the antimicrobial, antibacterial agent FALL-39 (see AAR92923). It is the product of a cDNA clone (AAT18233) isolated from a human bone marrow cDNA library. FALL-39 includes a helical region (see AAR92922) that is required for biological activity. FALL-39 is useful therapeutically for inhibiting microbial growth in mammmals, including humans, and is non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDPRPTWDGDPDTPKPVSFTVKETVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDPRPTMDGDPDTPKPVSFTVKRTVCPRTTQQSPRDCDPKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                     peptide antibiotic, FALL-39 - overcomes classical antibiotic
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Pred. No. 1.4e-88;
1; Mismatches 0; Indels
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                                                                                                                      Gunne H;
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                                                                                                                                                                                                                                                                                                 resistance and is non-cytotoxic.
                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 1; 26pp; English
                                                                                                               Gudmundsson GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%;
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17-NOV-2000; 2000US-0249602P.
15-MAY-2001; 2001US-0290932P.
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94SE-00003055
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                                                                                                                                                                          WPI; 1996-179899/18.
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Best Local Similarity
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G
                                                                                                                                                                                                      N-PSDB; AAT18233
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Thorton SL;

Hirsch R,

2003-712740/67.

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The invention describes new transplant compositions comprising antimicrobial polypeptides or pore forming agents and/or cell surface creceptor binding compounds. The media is capable of extending the preservation period past 72 hours and can provide organs with increased functionality upon transplant, animals receiving kidneys stored in the media of the present invention for either three or four days had serum creatinine levels of less than half of those observed in control animals receiving kidneys stored in UW solution (defined in the specification) alone. Lower serum creatinine levels are indicative of healthier kidneys alone. Lower serum creatinine levels are indicative of healthier kidneys can amore preferable prognosis for the transplant patient. The media of the invention are useful for decreasing the incidence and/or severity of delayed graft function in patients receiving transplant of healthier and/or treated in the media. The media may also be used in procedures such as cardioplegia. It is contemplated that transplant of healthier organs leads to a decrease in chronic rejection. This sequence represents an antimicrobial peptide studied in the development of the transplant
                         Media comprising antimicrobial polypeptides or pore forming agents and/or cell surface receptor binding compounds useful for the storage and preservation of organs prior to transplant.
                                                                                                                                                   Disclosure; Page 27; 78pp; English.
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LDPRPTMDGDPDTPKPVSFTVKGTVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120 1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 1 MKTQRNGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD LDPRPTMDGDPDTPKPVSFTVKRTVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS ; 0 PDISCONONICRPALLGOPPRKSKEKIGKEFKRIVQRIKOPLRNLVPRTES 170 Length 170; Score 874; DB 5; Length 17 Pred. No. 1.4e-88; 1; Mismatches 0; Indels 99.48; 99.44; Local Similarity 99.4 nes 169, Conservative Sequence 170 AA; 61 61 121 121 Query Match Best Loca Matches ò 셤 ઠે 윱 ò

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Gaps

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autoimmune disease; arthritide; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antijout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; Fibrositis; fibromyalgis; osteoarthritis; gout; juvenile rheumatoid arthritis; Human cathelicidin antimicrobial peptide. ADP65263 standard; protein; 170 AA (first entry) immune; human 12-AUG-2004 ADP65263; RESULT 10

31-OCT-2002; 2002WO-US035433. WO2003072827-A1. Homo sapiens 04-SEP-2003

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

31-OCT-2001; 2001US-0336220P.

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C gene expression signature of the marky, and using that c free free autofumune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention of further comprises: a treatment of theumatoid arthritis; identification of further comprises: a treatment of rheumatoid arthritis; identification of coher than a mouse; diagnosis of freumatoid arthritis in a mammal of array or gene chip, specific for rheumatoid arthritis; dangnosis or analyses of autoimmune disease or rheumatoid arthritis; dangnosis or analyses of autoimmune disease or rheumatoid arthritis; dangnosis or induced arthritis; and reducing the symptoms associated with collagentinduced arthritis; under compositions of the present invention are useful for artigout, autinitiammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for theumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, and an immune disease caused by an infectious agent. This sequence repartment of immune disease or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from
                                                                                                                                   Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
                                                                                                                                                                                                                                                                                                                                                              autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that
                                                                                                                                                                                                                                                                                                                                         invention relates to a novel method for diagnosing and analysing
                                                                                                                                                                                                                                                                                      Disclosure; Page; 56pp; English.
                                                                                GENBANK; NP_004336.
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120 61 LDPRPIMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLLNQARGS 120 9 9 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD Gape ö PDISCDKONKRPALLGDPPRKSKEKIGKEPKRIVQRIKDPLRNLVPRTES Length 170; 0; Indels Score 874; DB 7; Pred. No. 1.4e-88; 1; Mismatches 0 99.4%; Best Local Similarity 99.4 Matches 169; Conservative 121 19 Query Match 8 셤 8 셤 ò

Sequence 170 AA;

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infection, cathelicidin type peptide; LL-37; antimicrobial; antiinflammatory; immunostimulant; bacterial infection; neutropenia; toothpaste; mouthwash; ginglvitis; oral infection; periodontitis; human. PDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTBS 170 ADN41827 standard; protein; 170 Human LL-37 protein SEQ ID NO:2. 15-JUL-2004 (first entry) ADN41827; 121 RESULT 11 ADN41827 ID ADN g

Ното варіепв

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                  The present invention describes a method for determining the susceptibility of a subject to infection. The method comprises: (i) gusceptibility of a subject to infection. The method comprises: (i) providing a sample from a subject; (ii) detecting any cathelicidin type comported (LL-37) present in the sample; (iii) optionally comparing the susceptibility of the subject to infection (where no LL-37 or a low level of LL-37 indicates that subject is susceptible to infection); and (v) of LL-37 indicates that subject is susceptible to infection; and (v) optionally administering an antimicrobial agent to reduce infection. Also described is a product containing LL-37 and a cytostatic drug, corticosteroid or growth factor (Greferably recombinant granulocyte colony stimulating factor (G-CSF) or GM-CSF). The product has continicobial, antilinfammatory and immunostimilant activities. The method can be used for determining the susceptibility of a subject to infection such as bacterial infection (e.g. Actinobacillus cationomycetemocomitans infection) and neutropeabalia, and for diagnosing cationomycetemocomitans infection) and neutropeabalia, and for diagnosing neutropeabalia, and for diagnosing cationomycetemocomitans infection e.g. singivitis, oral infection (such as periodontties), and for the presente invention of human LL-37, which is used in the exemplification of the present invention invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour-associated antigenic target (TAT) polypeptide PR036373, SEQ:1129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LDPRPTWDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                     Determination of susceptibility of subject to infection comprising
                                                                                                                                                                                                                                     detecting cathelicidin type peptide present in sample, optionally comparing level of peptide in sample to control sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDISCDKDNKRFALLGDPFRKSKEKIGKBFKRIVQRIKDFLRNLVPRTES 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.4%; Score 874; DB 8; Length 170
99.4%; Pred. No. 1.4e-88;
ive 1; Mismatches 0; Indels
                                                                                                                                                 Carlsson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention.
                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 2; 40pp; English.
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                                                                                                                                                    Puetsep K,
                                                                  10-OCT-2003; 2003WO-EP011240.
                                                                                             10-OCT-2002; 2002GB-00023655
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                                                                                                                                                   Andersson M,
                                                                                                                                                                              2004-364936/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                         (MABT-) MABTECH AB
                                                                                                                                                                                          N-PSDB; ADN41826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 170 AA;
             WO2004034061-A2.
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                                       22-APR-2004
                                                                                                                                                    Boman H,
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the interaction retailed to mountain commonstance animogenic deader. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide cancer in mammals. The invention also relates to nucleic acid and polypeptide equences at least 80% identical to the TAT nucleic acids and nucleic acids, an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagoniers, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with concers, lung cancer, colorected cancer, lung cancer, cancer, succers of the central cancer, lung cancer, cancers of the central cancer, lung cancer, cancer, some system melanoms and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDPRPTMDGDPDTPKPVSFTVKRTVCPRTTQQSPRDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human tumour-associated antigenic target (TAT)
       cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acids,
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Tumour-associated antigenic target; TAT; human; overexpression; ctumour; diagnosis; cell proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; cervical cancer; melanoma; leukaemia; hybridisation probe; chromosome identification; chromosome mapping; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDISCDKDNKRFALLGDFFRKSKEKIGKBFKRIVQRIKDFLRNLVPRTES 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tumor-associated antigenic target polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; SEQ ID NO 1129; 7273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-2002; 2002US-0414971P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-2003; 2003WO-US028547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prostate cancer or tumor.
                                                                                                                                                                                                                                  gene therapy; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3est Local Similaricy 33.3
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACN37923
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                                                                                                                                                                                                                                                                                                                                                                               WO2004030615-A2
                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Keratinocyte growth factor-2 (KGP-2) (1) comprising heterologous keratinocyte growth factor-2 (KGP-2) (1) comprising providing a host cell (1) consisting of primary keratinocytes and immortalized keratinocytes and an expression vector comprising a DNA sequence encoding (1) operably control con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Providing cells expressing heterologous keratinocyte growth factor-2 (I), which is useful to treat wounds e.g. ulcerative colitis, comprises introducing a vector comprising a DNA that encodes (I) to a host cell and culturing the host cell.
                                                                                                                                                                                                                         vulnerary; antiulcer; antiinflammatory; gastrointestinal-gen.;
expression; vector; wound healing; vulnerary; injury; antimicrobial.
                                                                                                                                                                               Cathelicidin antimicrobial peptide SEQ ID NO 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 47; 116pp; English
                                            ADX08374 standard; protein; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centanni JM, Allen-Hoffmann L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-2003; 2003US-0491869P.
08-AUG-2003; 2003US-0493664P.
30-JUL-2004; 51US-00493664.
                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2004; 2004WO-US024627.
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (STRA-) STRATATECH CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-142888/15.
                                                                                                                                                                                                                                                                                                                                         WO2005012492-A2
                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                  21-APR-2005
                                                                                                                                                                                                                                                                                                                                                                                     10-PEB-2005
                                                                                        ADX08374;
RESULT 13
                       ADX0837
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The invention relates to a method of inhibiting the spread and/or reducing the risk of infection of a virus, involving contacting a virus with a cathelicidin functional fragment. The invention also relates to a method of treating atopic dermatitis involving contacting a subject having or suspected of having acopic dermatitis with an inhibiting effective amount of a cathelicidin functional fragment. The cathelicidin functional argament. The cathelicidin antiviral activity. The methods are useful for inhibiting the spread and/or reducing the risk of infection of a virus and for treating atopic dermatitis. This sequence represents the human cathelicidin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting spread and/or reducing risk of infection of virus, involves contacting virus with cathelicidin functional fragment.
                                                                                1 MKTQRNGHSLGRWSLVLLLLGLWPPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                             1 MKTQRDGHSLGRWSLVLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Infection, viral infection, cathelicidin, atopic dermatitis; antimicrobial; virucide; dermatological; dermatological disease; immune disorder; inflammation.
                                                                                                                                                                                        170
                                                                                                                                                                                                    PDISCDKDNKRFALLGDFFRKSKEKIGKEPKRIVQRIKDFLRNLVPRTES 170
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                                                                                                                                                                                        FDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES
Length 170;
99.4%; Score 874; DB 9; Length 17
99.4%; Pred. No. 1.46-88;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note≈ "Encoded by GAT'
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(NAJE-) NAT JEWISH MEDICAL & RES CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                ADZ80363 standard; protein; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leung DYM;
                                                                                                                                                                                                                                                                                                                                                                                           Human cathelicidin polypeptide.
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
                 Best Local Similarity 99.4 Matches 169; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-355820/36.
              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2005040201-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              14-JUL-2005
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   Query Match
                                                                                                                                                                                                                                                                   RESULT 14
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Sequence 170 AA;

antimicrobial peptide of the invention.

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                                                                                                                                                          61 LDPRPTWDGDPDTPKPVSFTVKBTVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                         LDPRPTWDGDPDTPKPVSFTVYGTVCPRTTQQSPEDCDPKKDGLVKRCMGTVTLNQARGS 120
                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vaccine for active immunization or for preparing an adjuvant for enhancing an immune response to at least one antigen, comprises at least one antigen and at least one cathelicidin derived antimicrobial peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine, cathelicidin; antimicrobial; immunostimulant; immune response; antigen presenting cell; adjuvant; human; antibiotic; FALL-39.
                                                                                        1 WKTQRNGHSLGRWSLVLLLGLWWPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                                     1 MKTORDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                    Gaps
                                                                                                                                                                                                                                  121 FDISCDKONKRPALLGDFFRKSKRKIGKRFKRIVQRIKDFLRNLVPRTBS 170
                                                                                                                                                                                                               121 PDISCDKDNKRPALLGDPFRKSKEKIGKBFKRIVQRIKDFLRNLVPRTBS 170
                                    ;
0
 Length 170;
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                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buschle M, Egyed A;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human peptide antibiotic FALL-39 precursor sequence.
99.4%; Score 874; DB 9;
ilarity 99.4%; Pred. No. 1.4e-88;
Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%; Score 865; DB 5;
98.8%; Pred. No. 1.4e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CIST-) CISTEM BIOTECHNOLOGIES GMBH
                                                                                                                                                                                                                                                                                                                                       ABB07707 standard; peptide; 170 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fritz J, Mattner F, Zauner W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-2000; 2000AT-00001416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-AUG-2001; 2001WO-EP009529
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-269154/31.
Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200213857-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                            10-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FBB-2002
                                                                                                                                                                                                                                                                                                                                                                          ABB07707;
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Best Local S
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Gaps

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1; Indels

1; Mismatches

Best Local Similarity 98.8 Matches 168; Conservative

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PDISCDKONKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170 121 PDISCDKONKRFALLGDFFRKSKEKIGKBFKRIVQRIKDELRNLVPRTES 170 121 ઠે ద ò a

Search completed: January 12, 2006, 21:48:09 Job time : 92.3321 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

January 12, 2006, 21:43:14; Search time 15.0554 Seconds (without alignments) 1086.448 Million cell updates/sec US-10-815-562-2

879 1 MKTQRDGHSLGRWSLVLLLL.....KRIVQRIKDFLRNLVPRTES 170 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
!: pir1:*
!: pir2:*
!: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

				pept	ccha	pept	prot	pept	pept	ed p	-2) p	scure	prot	recur	precur	precur	precur	recur	precu	d par	recur	crop	ed p	anti	pept	_	lear	lear	phopr	I'MM II	
		Description	CAP18 precursor	antibacterial	18K lipopolysaccha	antibacterial	antibacterial	antibacterial	antimicrobial	cathelin-related p	prophenin (PF-2)	bactenecin precurs	antimicrobial prot	protegrin 5 precur	protegrin 2 p	protegrin 3 p	protegrin 1 p	protegrin 4 precur	bactenecin 5 precu	cathelin-related p	indolicidin precur	myeloid antimicrob	cathelin-related p	cathelin-like anti	antimicrobial pept	cathelin - pig	polymorphonuclear	polymorphonuclear	secreted phosphopr	kininogen, LM	Take to a contract to the total
SUMMARIES			138932	S74248	101171	268967	2 \$41731	: A53421	868229	S70521	S40463	S27018	S68232	857609	2 JN0900	. A53895	. 857607	B53895	. A45328	S68412	JC1222	S68228	S68411	857330	: S68230	XKPGC	: B46634	: A46634	146051	KGBOL2	210000
		Match Length DB	170	170	171	167	166	153	155	173	228	155	172	149	•	149	149	149	176	160	144	160	152	212	190	96	135	137	200	434	
	onerv	Match	100.0	99.4	53.0	50.6	50.5	49.9	49.2	49.1	48.9	48.6	48.6	48.3	47.6	47.6	47.6	47.6	46.7	46.2	46.1	45.4	45.1	44.1	42.6	36.3	19.6	19.5	7.6	7.6	c
		Score	879	874	465.5	444.5	443.5	438.5	432.5	431.5	429.5	427.5	427.5	424.5	418.5	418.5	418.5	418.5	410.5	406	405.5	399	396	387.5	374.5	319	172.5	171.5	85.5	85	40
	Result	No.	-	7	e	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	000

kininogen, LMW I p kininogen, HMW I p	hypothetical prote	spp-24 precursor -	hypothetical prote	lipoxygenase (EC 1	serine/threonine p	ATPase 2 (EC 3.6.1	hypothetical prote	f22b7.6 protein -	CTP synthetase ctr	hypothetical prote	hypothetical prote	FixL Oxygen regula	nitrogen fixation	hypothetical prote
KGBOL1 KGBOH1	AC1435	G01654	C84397	A53054	T50802	T31112	T18804	844637	H84123	T20566	F84680	F95345	S39984	T15854
н н	7	~	N	~	~	~	~	~	N	~	~	~	~	7
436 621	273	211	263	923	445	1082	444	518	532	2911	245	505	505	1599
9.0	4.6	9.3	9.0	9.0	8.9	8.9	8.8	8.8	8.8	8.8	8.7	8.5	8.5	8.5
84 84	82.5	82	79	79	78.5	78.5	77.5	77	77	77	76.5	75	75	75
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ALIGNMENTS

RESULT 1 138932 CAD18 precursor - human			
C:Species: Homo sapiens (man)			
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004	#text_change 09-Jul-20	104	
C;Accession: 138932	ı		
R; Larrick, J.W.; Hirata, M.; Balint, R.F.; Lee, J.; Zhong, J.; Wright, S.C.	Zhong, J.; Wright, S.	ů.	
Infect. Immun. 63, 1291-1297, 1995			
A; Title: Human CAP18: a novel antimicrobial lipopolysaccharide-binding protein.	ysaccharide-binding pr	otein.	
A; Reference number: I38932; MUID:95197251; PMID:7890387	0387		
A; Accession: 138932			
A;Status: preliminary; translated from GB/EMBL/DDBJ			
A; Molecule type: mRNA			
A;Residues: 1-170 <res></res>			
A; Cross-references: UNIPROT: P49913; UNIPARC: UP10000000A67; EMBL: U19970; NID: 9643476; PID	000A67; EMBL:U19970; N	IID:9643476;	PID
C;Superfamily: cathelin; cystatin homology			
F;22-130/Domain: cystatin homology <cys></cys>			

ö MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD Gaps ò Length 170; Indele ô 100.0%; Score 879; DB 2; 100.0%; Pred. No. 8.8e-77; ive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 170; Conservative Š

1 MKTQRDGHSLGRWSLVLLLGLGLVWPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD

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120 61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPBDCDPKKDGLVKRCMGTVTLNQARGS 19 g ò ઠે

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121 FDISCDKONKRPALLGDFFRKSKEKIGKEFKRIVQRIKDFLANLVPRTES 170 121 PDISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170 셤

Nylternate names: antibacterial peptide FALL39
Nylternate names: antibacterial peptide FALL39
Nylternate names: antibacterial peptide FALL39
Nylontains: antibacterial peptide LL-37; cathelin-related antibacterial peptide CAP-18
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S74248; S78211; S66281; S66281; S65285; S49441; S58023
R;Gudmundsson: G.H.; Agerberth, B.; Odeberg, J.; Bergman, T.; Olsson, B.; Salcedo, R.
Bur. J. Blochem. 238, 325-332, 1996
A;Title: The human gene FALL39 and processing of the cathelin precursor to the antibacte A;Accession: S74248; MUID:96283824; PMID:8681941
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-170 cGUD>
A;Residues: 1-170 cGUD>
A;Accession: S78211

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A;Note: 157-Asp was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S41731
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          A MOLECULE LYPE: DIOCELIN
A FROSIDATE LYPE: JOHNSON, A.H.; BOTTEGBARG, N.
A; CTOGE-TETEFRACE LYPE: J. 1. 21. 21. 61. 995;
A; CTOGE-TETEFRACE LYPE: DECEDIAL SEGUES, MUDI-95339969; PMID: 7615076
A; Reference number: S66205; MUDI-95339969; PMID: 7615076
A; Reference number: S66205; MUDI-95339969; PMID: 7615076
A; Reference number: S66205; MUDI-95339969; PMID: 7615076
A; Residues: 1.1.2. TT., 1.1.4. 1.70 < COOM-A; Residues: UNIPARC: UPIO000000667; RMB-1, S00-100, 1110-112, TT., 1.1.4-122 < COCP-A; CTOGE-TETEFRACE LYPE: DIAMAC: UPIO00017636F; UNIPARC: UPIO00017636F; UNIPARC: UPIO00017630F; M. S. P. S2. 1.3. 1.5. 1.95-1.99; 1.995
A; TILLE: FALL-19, a putative human peptide antibiotic, is cytetine-free and expressed in A; Reference number: A55596; MUDI-9516523; PMID: 7529412
A; Reference number: A55596; MUDI-9516523; PMID: 7529412
A; Reference number: A55596; MUDI-9516523; PMID: 7529412
A; Reference number: A55596; MUDI-9516523; PMID: 7529412
A; Reference number: A55596
A; Reference num
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NyAlternate names: 18K cationic protein
C;Specias: Orytoolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
C;Accession: JQ1171; PS0226
C;Accession: JQ1171; PS0226.; Palings, I.; Hirata, M.; Yen, M.H.
B;Cochem. Biophys. Res. Commun. 179, 170-175, 1991
B;Cochem. Biophys. Res. Commun. 179, 170-175, 1991
B;Cochem. Biophys. Res. Commun. 179, 170-175, 1991
B;Cochem. Biophys. Res. JQ1171; MUD:91354246; PMID:1883348
A;Recession: JQ1171; MUD:91354246; PMID:1883348
A;Accession: JQ1171 MUD:91354246; PMID:1883348
A;Accession: PS026
A;Molecule type: MIPPARC:UPI0000145211
A;Experimental source: bone marrow
A;Accession: PS0226
A;Molecule type: protein
A;Residues: 135-159, OGGQLL' <LA2>
A;Cross-references: UNIPPARC:UPI0000176372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.4%; Score 874; DB 2; Best Local Similarity 99.4%; Pred. No. 2.7e-76; Matches 169; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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antibacterial peptide - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus Scr-1996 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S68967
R;Tossi, A.; Scocchi, M.; Zanetti, M.; Storici, P.; Gennaro, R.
R;Tossi, A.; Scocchi, M.; Zanetti, M.; Storici, P.; Gennaro, R.
A;Title: PWAP-37, a novel antibacterial peptide from pig myeloid cells. cDNA cloning, change presence number: S68967
A;Reference number: S68967
A;Accession: S68967
A;Status: preliminary
A;Accession: Preliminary
A;Residues: 1-167 <TOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P49932; UNIPARC:UPI000012F429; EMBL:L39641; NID:G703244; PID:C;Superfamily: cathelin; cystatin homology
F;22-129/Domain: cystatin homology <CYS>
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Cispecies: Sus scroca domestica (domestic pig)
Cjate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
CjAccesion: 841731
RiStorici, P.; Scocchi, M.; Tossi, A.; Gennaro, R.; Zanetti, M.
Ristorici, P.; 303-307, 1994
A;Title: Chemical synthesis and biological activity of a novel antibacterial peptide ded
A;Reference number: 841731; MUID:94123775; PMID:8293820
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A;Rosidues 1.166 cSTO-
A;Gross-references: UNIRROT:P49931; UNIPARC:UP1000012F428; GB:L29125; NID:g457347; PIDN:
C;Superfamily: cathelin; cystatin homology
C;Superfamily: cathelin; cystatin homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                              60 MDPQQLEDAKPYTPQPVSFTVKETECPRTTWKLPEQCDFKEDGLVKRCVGTVTRYQAWDS 119
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                                                                                                                                                                                                                                                                     1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                   Gaps
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                                                                                                                                    DB 2; Length 171;
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120 LDITCNBIQSVGLLSRLRDFLSDRGRRLGEKIERIGQKIKD 160
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                                                                                                                             Query Match
53.0%; Score 465.5; DB 2
Best Local Similarity 57.3%; Pred. No. 3.5e-37;
Matches 98; Conservative 26; Mismatches 44
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C;Date: 15-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Caccession: S70521
R;Popueva, A.E.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlmans, J.M.J.M.; Fibbe, W.E.; Bely
PEBS Lett. 391, 5-8, 1996
A;Title: A novel murine cathelin-like protein expressed in bone marrow.
A;Reference number: S70521; MUID:96326596; PMID:8706928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reaidues: 1-173 <POP>
A;Reaidues: 1-173 <POP>
A;Cross-references: UNIPROT:P51437; UNIPARC:UPI000049482; EMBL:X94353; NID:g1177533; PI
C;Superfamily: cathelin; cystatin homology
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-144/Domain: propeptide #status predicted <PRO>
F;145-173/Product: cathelin-related protein #status predicted <MAT>
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NyAlternate names: antimicrobial peptide; cathelin-like antibacterial peptide precursor Sispecies Sus acrofa domestica pig)
C;Species Sus acrofa domestica (domestic pig)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 840463; 857331; §6823
C;Accession: 840463; 857331; §6823
A;Pungercar, J; Strukelj, B.; Kopitar, G.; Renko, M.; Lenarcic, B.; Gubensek, P.; Turk, PEBS Lett. 336, 284-288, 1993
A;Title: Molecular cloning of putative homolog of proline/arginine-rich antibacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cathelin-related protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                        58 LDPEPQGDEDPDTPKSVRFRVKETVCGKAERQLPEQCAFKEQGVVKQCMGAVTLNPAADS
                                                                                                                                                                                                                                                                    1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                  Length 155;
P;22-129/Domain: cystatin homology <CYS>
P;29-143/Domain: propeptide #status predicted <PRO>
P;144-155/Product: antimicrobial peptide #status predicted <MAT>
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                                                                                                                                     DB 2;
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18; Mismatches 21
                                                                                                                                         Score 432.5;
                                                                                                                                     49.2%;
                                                                                                                                                                         68.3%;
                                                                                                                                                                                                        86, Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
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antibacterial peptide precursor - pig
antibacterial peptide precursor - pig
antibacterial peptide domestica (domestic pig)
C;Specials B scrofa domestica (domestic pig)
C;Bate: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: A53421
B;Zaneti, M.; Storici, P.; Tossi, A.; Scocchi, M.; Gennaro, R.
J. Biol. Chem. 269, 7855-7858, 1994
A;Title: Molecular cloning and chemical synthesis of a novel antibacterial peptide deriv
A;Recession: A53421
A;Accession: A53421
A;Accession: Barlahnary
A;Molecule type: mRNA
A;Residues: 1-153 < ZAN
A;Coss-references: UNIPROT:P49930; UNIPARC:UP1000012F425; GB:L26053; NID:g468911; PIDN:
C;Superfamily: cathelin; cystatin homology
C;Superfamily: cathelin; cystatin homology
C;Superfamily: cathelin; Cystatin homology
C;Superfamily: Cathelin; Cystatin homology
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NyAlternate names: procyclic dodecapeptide homolog

Cispecias: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

Cispecias: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

Cispecias: Ovis orientalis aries, Ovis ammon aries

Cispecias: Ovis orientalis aries, Ovis ammon aries

Cispecias: Ovis orientalis aries, Ovis ammon aries

Cispecias: Ovis orientalis

Risagella, Liscocchi, M.; Zanetti, M.

Risagella, Liscocchi, M.; Zanetti, M.

Risagella, Liscocchi, M.; Zanetti, M.

A;Reference number: S68228, MUID:96105386; PMID:7498547

A;Reference number: S68228, MUID:96105386; PMID:7498547

A;Reterence number: S68
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                                                                          Length 166;
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                                                               Query Match 50.5%; Score 443.5; DB 2; Best Local Similarity 61.3%; Pred. No. 4.3e-35; Matches 95; Conservative 18; Mismatches 39;
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Best Local Similarity 67.7%; Pred. No. 1.2e-34,
Matches 86; Conservative 19; Mismatches 21
   F;22-129/Domain: cystatin homology <CYS>
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P;144-155/Product: bactenecin #status experimental <MAT>
P;146-154/Disulfide bonds: #status experimental
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A;Strukelj, B.; Pungercar, J.; Kopitar, G.; Renko, M.; Lenarcic, B.; Berbic, S.; Turk, V. Biol. Chem. Hoppe-Seyler 376, 507-510, 1995

Biol. Chem. Hoppe-Seyler 376, 507-510, 1995

A;Title: Molecular cloning and identification of a novel porcine cathelin-like antibacte A;Reference number: S57330; MUD:96042752; PMID:7576250

A;Attle: Molecular cloning and identification of a novel porcine cathelin-like antibacte A;Reference number: S57330; MUD:96042752; PMID:7576250

A;Accession: S57331

A;Status: preliminary

A;Molecule type: mNNA

A;Residues: 1-228 «STR»

A;Cross-references: UNIPARC:UPI0000131713

R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FBBS Lett. 376, 130-134, 1995

A;Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen A;Reference number: S68233

A;Status: preliminary

A;Accession: S6823

A;Residues: 1-228 «ZHA»

A;Residues: 66/3; 102/3; 126/3

C;Superfamily: cathellin, cystatin homology

F;1-29/Domain: signal sequence #status predicted «MAT»

F;22-129/Domain: cystatin homology «CYS»

F;30-228/Product: prophenin (PP-2) #status predicted «MAT»
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Bactemedin precursor - bovine

NyAlternate names: antibiotic dodecapeptide
C;Species: Bos primigraphius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: 237018; A33799
R;Storici, P.; del Sal, G.; Schneider, C.; Zanetti, M.
FEBS Lett. 314, 187-190, 1992
A;Title: CDMS sequence analysis of an antibiotic dodecapeptide from neutrophils.
A;Reference number: S27018; MUID:93093170; PMID:1459251
A;Residues: 1-155 csTO-
A;Ccession: S27018
A;Molecule type: mRNA
A;Residues: 1-155 csTO-
A;Cross-references: UNIPROT:P22226; UNIPARC:UP10000049485; GB:L08834; NID:9162599; PIDN:
A;Residues: 1-155 csTO-
A;Cross-references: UNIPROT:P3799; MUID:88257074; PMID:3290210
A;Title: Structure and bacteridad activity of an antibiotic dodecapeptide purified from A;Residues: 144-155 cstOM-
A;Residues: 144-155 cstOM-
A;Residues: 144-155 cstOM-
A;Residues: 144-155 cstOM-
A;Residues: 144-155 cstOM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 48.9%; Score 429.5; DB 2; Best Local Similarity 60.1%; Pred. No. 1.4e-33; Matches 86; Conservative 23; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDISCDKDNKRFALLGDFFRKSK 143
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A/Title: Structures of genes for two cathelin-associated antimicrobial peptides: prophen A/Reference number: S68232; MUID:96105365; PMID:7498526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosicule type: DNA
A;Mosicule type: LNA
A;Cross-references: UNIPROT:P80054; UNIPARC:UPI000013215A; EMBL:X89201; NID:gl165150; PI
A;Experimental source: leukocytes
R;Storici, P.; Zanetti, M.
Bjochen: Biophys: Res. Commun. 196, 1058-1065, 1993
A;Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to the A;Reference number: JN0899; MUID:94071853; PMID:8250863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA.

A; Molecule type: DNA.

A; Moseidues: 1-28, "T',30-99, 'QR', 92-116,' NDP',120-172 <GUD>
A; Cross-references: UNIPARC: UPIO00016C6AC; EMBL: K87236; NID: 9829142; PIDN: CAA60682.1; PI R; Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall R; Agerberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Boman, H.G.; Mutt, V.; Joernvall Br.; J. Blochem. 202, 849-854, 1991

A; Title: Amino acid sequence of PR-39. Isolation from pig intestine of a new member of this Rsteference number: S19563; MUID: 92111534; PMID: 1765098
                                                                                                                                                                                                                                                                 61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDPKXDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                      60 LDQPPQDDBDPDSPKRVSPRVKETVCSRTTQQPPEQCDFKENGLLKRCEGTVTLDQVRGN 119
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NyAlternate names: myeloid antibacterial protein PR-39
C;Species: Sus scroff domestica (domestic pig)
C;Date: 15-Feb-1997 #sequence revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68232; JN0899; I47138; S19563
R;Zhao, C; Ganz, T; Lehrer, R.I.
R;Zhao, C; Ganz, T; Lehrer, R.I.
A;Fille: Structures of genes for two cathelin-associated antimicrobial pepti
                                                                                                                                                                    1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
                                                                 Gaps
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C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated cathoxyl end; antibacterial
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>
                                                                 .,
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   Length 155;
                                                                 Indels
   DB 2;
                                     pred. No. 1.4e-33;
18; Mismatches 23;
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Score 427.5;
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Mresidues: 131-159 cAGES
A;Cross-references: UNIPARC:UP1000002D613
A;Experimental source: intestine
      48.64;
                                     66.78;
                                                                 84; Conservative
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                                     Best Local Similarity
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A; Molecule type: mRNA
A; Residues: 1-147 <STO>
A; Cross-references: UNIPROT: P32195; UNIPARC: UPI0000131776; GB: L24745; NID: g431435; PIDN:
R; Mirgorodskaya, O.A.; Pevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A; Reference number: S36820; MUID: 93387466; PMID: 8375505
                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: protein

A,Residues: 13.1-146 AMIN.

A,Ecrodues: 13.1-146 AMIN.

B, Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; Sh.

B, Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; Sh.

B, Kokryakov, V.N.; 1993

A,Title: Protegrina: leukocyte antimicrobial peptides that combine features of corticost A,Reference number: S34585; MUID:93327946; PMID:8335113
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A; Residues: 131-146 <KOK>
A; Residues: 131-146 <KOK>
A; Cross-references: UNIPARC:UP1000014310F
A; Cross-references: UNIPARC:UP1000014310F
C; Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanism C; Superfamily: cathelin; cystatin homology
C; Keywords: amidated carboxyl end; antibacterial; neutrophil
F; 1-29/Domain: signal sequence #status predicted <SIG>
F; 1-29/Domain: cystatin homology <CYS>
F; 131-146/Product: protegrin 2 #status experimental <MAT>
F; 131-146/Product: amidated carboxyl end (Val) (amide in mature form from following gl
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A;Cross-references: UNIPARC:UPI0000131777; GB:X83267; NID:g603037; PIDN:CAA58240.1; PID:
R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; Sh
FEBS Lett. 327, 231-236, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LDPRPTMDGDPDTPKPVSFTVKGTVCPRTTQQSPBDCDFKXDGLVKRCMGTVTLNQARGS 120
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NyAlternate names: neutrophil peptide 2
Cispecies: Sus scroff domestica (domestic pig)
Cispecies: Sus scroff domestica (domestic pig)
Cispecies: Sus scroff domestica (domestic pig)
Cistecession: S66285; A53895; S34587; S36821; S57608
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
PEBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUD:95384835; PMID:7628604
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A; Reference number: JN0900; MUID:94071898; PMID:8250892
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47.6%; Score 418.5; DB 2
Best Local Similarity 65.4%; Pred. No. 9.3e-33;
Matches 83; Conservative 19; Mismatches 24
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A; Residues: 1-149 <ZH3>
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S55609
protegrin 5 precursor - pig
N;Alternate names: cathelin-associated antimicrobial peptide
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S6628; S7609
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1985
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUD:95354835; PMID:7628604
A;Reference number: S66283; MUD:95354835; PMID:7628604
A;Reference number: S66283, MUD:95354835; PMID:7628604
A;Residues: 1-149 <ZHA>
A;Residues: 1-149 <ZHA
A;Residues: 1-149 <ZH
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Nighternate names: catchelin-like protein precursor; neutrophil peptide 3
Nighternate names: catchelin-like protein precursor; neutrophil peptide 3
Cipteries: Sus scrofa domestica (domestic pig)
Cipteries: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
Cipteries: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
Ristorici, P.; Zanetti, M.
Biochem: Blophys. Res. Commun. 196, 1363-1368, 1993
A;Title: A novel CDNA sequence encoding a pig leukocyte antimicrobial peptide with a cad
    F;169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                 Gaps
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48.3%; Score 424.5; DB 2; Length 149;
Best Local Similarity 66.1%; Pred. No. 2.5e-33;
Matches 84; Conservative 19; Mismatches 23; Indels 1.
                                                                                        DB 2; Length 172;
                                                                                                                                                             Indels
                                                                                Query Match 48.6%; Score 427.5; DB 2;
Best Local Similarity 67.7%; Pred. No. 1.5e-33;
Matches 86; Conservative 17; Mismatches 23;
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120 LDISCNE 126
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120 LDITCNE 126
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rch completed: January 12, 2006, 21:51:07 time : 16.0554 secs
                       FEBS Lett. 327, 231-236, 1993
                                                                                                                                                              A; Accession: S34585
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A; Reference number: S34585; MUID:93327946; PMID:8335113
A; Accession: S34587
A; Accession: S34587
A; Accession: S34587
A; McCoule type: protein
A; Residues: 131-148 «KOX»
A; Cross-references: UNIPARC:UP10000143110
R; Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, FBS Lett. Primary structure of three cationic peptides from porcine neutrophils. Sequence
A; Reference number: S36820; MUID:93387466; PMID:8375505
A; Reference number: S36820; MUID:93387466; PMID:837550
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A; Accession: S66284
A; Accession: S66284
A; Molecule type: DNA
A; Residues: 1-149 < ZHA
A; Cross-references: UNIPROT: P32194; UNIPARC: UP10000131775; EMBL: X84094; NID: G887642; PID
R; Zhao, C.; Liu, L.; Lehrer, R.I.
FRES Lett. 346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: S45712; MUID: 94283613; PMID: 8013647
A; Ritle: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: S45712; MUID: 94283613; PMID: 8013647
A; Residues: 1-149 < ZH2.
A; Molecule type: mRNA
A; Residues: 1-149 < ZH2.
A; Molecule type: MUID: 94283613; PMID: 8175968; NID: G603035; PIDN: CAA56251.1; PID: R; MITGOROGRAYA, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, FEBS Lett. 330, 339-342, 1993
A; Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence A; Reference number: S36820
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 131-148 < MIR.>
A; Rosidues: UNIPARC: UP10000034C2E
A; Rosidues: UNIPARC: UP1000034C2E
A; Rosidues: UNIPARC: UP1000034C2E
A; Rosidues: UNIPARC: UP1000034C2E
A; Rosidues: Millow A; Aleshina, G.M.; Shevchenko, A.A.; Aleshina, G.M.; Sh
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NiAlternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S66284; S45712; $36820; S34585; S57607
R;Zhao, C; Ganz, T.; Lehrer, R.I.
FBBS Lett. 368, 197-202, 197-202, 197-204
A;Ritle: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
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A,Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticost
A,Reference number: S34585, MUID:93327946; PMID:8335113
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Ajintrons: 66/3; 102/3; 126/3
C;Superfamily: cathelin; cystatin homology
C;Superfamily: cathelin; cystatin homology
C;Cysyonain: signal sequence #status predicted <81G>
F;1-29/Domain: signal sequence #status predicted <81G>
F;21-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>
F;111-148/Product: protegrin 1 #status experimental <PRO>
F;1148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LOPRPTWOGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                       A;Molecule type: protein
A;Meaidues: 131-148 «KOK»
A;Cross-references: UNIPARC:UPI0000034C2E
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 65.49
Matches 83; Conservative
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120 LDITCNE 126
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us-10-815-562-2.rup

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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OM protein - protein search, using sw model

January 12, 2006, 21:42:24; Search time 82.8044 Seconds (without alignments) 1448.471 Million cell updates/sec Run on:

US-10-815-562-2 879 1 MKTQRDGHSLGRWSLVLLLL......KRIVQRIKDFLRNLVPRTES 170 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 2166443 seqs, 705528306 residues Searched:

2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

otion	homo sapien		macaca mula	_	canis famil	oryctolagus	equus cabal	bos taurus	rattus norv	equus cabal	sus scrofa	sus scrofa	capra hircu	capra hircu	ovis aries	sus scrofa	ovis aries	mus musculu	ovis aries	bos taurus	bos taurus	capra hircu	sus scrofa	bos taurus	sus scrofa	bos taurus					
Description	P49913	Q718n9	Q9g1v5	062841	Q6tn20	P25230	062842	P56425	Q71km5	062840	P49932	P49931	P82018	Q4 j fb9	P79360	P49930	P79362	P51437	P54230	P54228	P54229	P82017	P51525	P22226	P80054	P49934	P32195	P32194	P32196	P49933	.P19661
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ID	FAL39_HUMAN	PAL39_MACMU	Q9GLV5 MACM	062841_HORSE	Q6TN20 CANFA	CAP18 RABIT	062842 HORSE	BMA34 BOVIN	Q71KM5 RAT	062840 HORSE	PMP37 PIG	PMP36 PIG	BCTN5 CAPHI	Q4JFB9 CAPHI	P79360_SHEEP	PMP23 PIG	BCTN5 SHEBP	CRAMP MOUSE	BCTV1 SHEEP	BMA27_BOVIN	BMA28 BOVIN	P82017 CAPHI	PF12 PIG		PR39 PIG	PG5_PIG	PG2_PIG	PG1_PIG	PG3 PIG	PG4 PIG	BCTN7_BOVIN
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å Query Match Length	170	170	170	157	172	171	170	165	171	156	167	166	176	176	165	153	176	173	155	158	159	165	228	155	172	149	147	149	149	149	190
& Query Match	100.0	100.0	86.3	56.7	55.3	53.3	52.0	51.6	51.6	51.3	50.6	50.5	50.3	50.3	50.1	49.9	49.8	49.3	49.2	49.1	49.1	49.0	48.9	48.6	48.6	48.3	47.6	47.6	47.6	47.6	47.4
Score	879	879	759	498.5	486.5	468.5	457.5		453.5	451	444.5	443.5	442.5	442.5	440	438.5	437.5	433.5	432.5	432	432	431	429.5	427.5	427.5	424.5	418.5	418.5	418.5	418.5	416.5
Result No.	п	7	m	4.	'nú	رود	7	8) .6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31

Q9xsq8 capra hircu P49928 ovis aries	P19660 bos taurus Q683r8 bubalus bub P11046 bos faurus	P49929 ovis aries P51524 sus scrofa	Q9xsq9 capra hircu P79361 ovis aries	P50415 ovis aries O19031 ovis aries	Ol9040 ovis aries Q91x12 cavia porce	Q920x4 mus spicile
Q9XSQ8 CAPHI SC51 SHEEP	BCTNS BOVIN Q683R8 BUBBU TNDC BOVIN	SC52_SHEEP PF11_PIG	Q9XSQ9_CAPHI P79361_SHEEP	BCTN7 SHEEP 019031 SHEEP	O19040 SHEEP Q91X12_CAVPO	Q920X4_MUSSI
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158 160	176	160	190 164	190	182 178	109
47.0	46.2	45.5	43.9	42.6	41.0 37.0	36.7
413	406.5	400	385.5	374.5 369.5	360.5 325	322.5
33 33	35	37	39 40	41	4 4 4	45

ALIGNMENTS

RESULT 1 19.199 AC P49913 AC P49913 AC P49913 DD 10-OCT DT 01-OCT DT 01-OCT DE CALLDO DE Antiba DE Antiba DE Antiba DE CALLO DE RAMMANDI DE CALLO DE RAMMANDI DE CALLO DE CALL
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HGNC; HGNC:1472; CAMP.

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MUCLECOTIDE SEQUENCE [LARGE SCALE MRNA].

MUCLECOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242699;

MEDLINE=22388257; PubMed=12477932;

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                                                                                                                                                                                                                                                                                                                                                                                                                    Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S., Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W., Koan B., Zuo D., Hu Y., Labaer J., "Cloning of human full open reading frames in Gateway (TM) system entry vector (pDONR201)."
"The human gene FALL39 and processing of the cathelin precursor to the antibacterial peptide LL-37 in granulocytes."; Eur. J. Biochem. 238:325-332(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial activity.
SUBCELLULAR LOCATION: Secreted.
TISSUB SPECIFICITY: Expressed in bone marrow and testis and
                                                                                                                                                                                                                                                                                      Wu N., Miao S.Y., Zhang X.D., Qiao Y., Liang G., Wang L.F.; "A new spermatogenesis-related gene."; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                             TISSUE=Epididymis;
Gao Y., Huang Y.F., Xia X.Y.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: The N-terminus is blocked.
SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238026; CAA86115.1; -; mRNA.
X89558; CAA61805.1; -; mRNN.
U19970; AAA74084.1; -; mRNA.
U19975; AAA702634.1; -; Genomic_DNA.
X96735; -; NOT_ANNOTATED_CDS; Genomic_DNA.
AY15210; AAN783181.1; mRNA.
AY251531; AAR2054.1; -; mRNA.
CR457083; CAG33364.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]
                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [MRNA].
                                                                                                       NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                TISSUE=Testis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
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PIR, 138932, 138932. PIR, S74248, S74248. HSSP, 923196, 1KWI. Ensembl, ENSG0000164047, Homo saplens.

CR541961; CAG46759.1; -; mRNA BC055089; AAH55089.1; -; mRNA

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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                 Pyrrolidone carboxylic acid (By similarity).
By similarity.
By similarity.
D -> N (in Ref. 1, 6, 7 and 8; CAG46759).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKTORDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [WRNA], AND TISSUE SPECIFICITY.

MEDLINE=21137962; PubMed=11238224; DOI=10.1128/CDLI.8.2.370-375.2001;
Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
Bals R., Lang C., Weiner D.J., Vogelmeier C., Welsch U., Wilson J.M.;
"Rheeus monkey (Macaca mulatta) mucosal antimicrobial peptides are
close homologues of human molecules.";
clin. Diagn. Lab. Immunol. 8:370-375(2001).

-! FUNCTION: Binds to bacterial lipopolysaccharides (LPS), has
antibacterial activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-2005 (Rel. 47, Last sequence update)
11-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial protein FALL-39 protein (RAL-39 peptide antibiotic)
(Cationic antimicrobial protein CAP-18) (rhCAP-18) [Contains:
Antibacterial protein LL-37 (rhLL-37)].
Antibacterial protein RP-18 (RAL-38)
Mame=CAMP; Synonyme=CAP18 (RAL-37)].
Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Expressed in epithelia of various organs.
abundant peptide levels are found in organs lining outer or in body surfaces, such as organs of the respiratory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
Cercopithecidae, Cercopithecinae, Macaca.
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                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 879; DB 1; Length 170; 100.0%; Pred. No. 6.9e-76;
                                                                                                                                                                                                                        Antibacterial protein FALL-39. Antibacterial protein LL-37.
                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                           InterPro; IPR01894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
Probom; PR001893; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Antimicrobial; Direct protein sequencing; Pyrrolidone carboxylic acid; Signal.
SIGNAL
                                response to bacteria; TAS.
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10-MAY-2005 (Rel. 47, Last segu
13-SEP-2005 (Rel. 48, Last anno
                                                                                                                                                                                                                                                                                                                                              170 AA; 19301 MW;
                MIM; 600474; -.
GO; GO:0042742; P:defense
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170
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125
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132
134
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108
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Q71SN9;
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DISULPID
CONFLICT
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MOD_RES
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SIGNAL
      Matches
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062841 HOI
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062842 HOI
062841 HOI
063841 HOI
06
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MEDLINE=2141139; PubMed=11557457;

MEDLINE=2141139; PubMed=11557457;

MEDLINE=2141139; PubMed=11557457;

Anc. 45.10.2695-2702.2001;

Maring A., Lehrer R.I.;

"RL-37, an alpha-helical antimicrobial peptide of the rhesus monkey.";

Antimicrob. Agents Chemother. 45:2695-2702(2001).

EMBL: AF181954; AAG09440.1; -; mRNA.
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Buropean Bioinformatics Institute. There are no restrictions on as long as its content is in no way modified and this statement
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                                                                                EMBL; AP288284; AAG40802.1; -; mRNA.
InterPro; IPRO01894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
Propon; PD001838; Cathelicidin; 1.
PROSTE; PR00946; CATHELICIDINS 1.
PROSTE; P800947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidon; carboxylic acid; Signal.
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GO; GO:0006952; P:defense response; IEA.
GO; GO:0006913; P:response to pest, pathogen or parasite; IEA.
InterPro; IPR001894; Cathelicidin.
Pfam; PF00666; Cathelicidins; 1.
                                                                                                                                                                                                                                                                                          Potential.
Antibacterial protein FALL-39.
Antibacterial protein LL-37.
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 879; DB 1; Length 170; 100.0%; Pred. No. 6.9e-76; ive 0; Mismatches 0; Indels
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PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
SEQUENCE 170 AA; 18861 MW; 355AB3BFS10DBB83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    similarity).
055B07DCA95A7D16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Pred. No. 2.1e-64;
                                                                                                                                                                                                                                                                        Potential
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Matches 170; Conservative
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Best Local Similarity

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LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                      61 LDPRPIMDGDPDTPKPVSFTVKETVCPRTTQKSPEDCDFKEDGLVKRCVGTVILNQARDS 120
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                         1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB-Bone marrow;
MBDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto B.,
Zanetti M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
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GO; GO: 0005576; C: extracellular region; IEA.

GO; GO: 0005517; C: extracellular region; IEA.

GO; GO: 0005613; P: defense response; IEA.

InterPro; IPR001894; Cathellicidin.

Probom; PP00666; Cathellicidins; 1.

Probom; PD001838; Cathellicidin; 1.

PROSITE; PS00946; CATHELLCIDINS 1; 1.

PROSITE; PS00947; CATHELLCIDINS 2; 1.
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                                                                                                                                                                                          Match 56.7%; Score 498.5; DB 2; Length Local Similarity 76.4%; Pred. No. 1.7e-39; Length 97; Conservative 13; Mismatches 16; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 24, Last annotation update)
My-Jun cathelicidin 2 precursor.
Name=eCATH-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Novel cathelicidins in horse leukocytes.";
FEBS Lett. 457:459-464(1999).
EMBL; AJZ24928; CAA12227.1; -; mRNA.
HSSP; P32196; IKWI.
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                                                                                                                                                                                                                                                                                                                                                                 O62841 HORSE PRELIMINARY;
062841;
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ID QGTN20 CANFA PRELIMINARY;
AC QGTN20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equus caballus (Horse).
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157
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PROTEIN SEQUENCE OF 135-154, AND CHARACTERIZATION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
                                                                   Cathelicidin.
Cania familiaris (Dog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Carnivora, Pissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1992 (Rel. 22, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A) [Contains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDISCDK--DNKRPALLGDPPRKSKEKIGKEPKRIVQRIKDFLRNLVPRTE 169
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Sang Y., Rune K., Melgarejo T., Blecha F.;
Sang Y., Rune K., Melgarejo T., Blecha F.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY392089; AAR52465.1; -; mRNA.
ENSCAFG0000012896; Canis familiaris.
GO; GO:000557; P:defense response; IEA.
GO; GO:0005512; P:response to pest, pathogen or parasite; IEA.
InterPro; IRRO01894; Cathelicidin.
Probom; PD001838; Cathelicidin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.3%; Score 486.5; DB 2; Length 172; 57.9%; Pred. No. 2.7e-38; ive 27; Mismatches 42; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=44178952; PubMed=8132348;
Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I.,
Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
"Characterization of a rabbit cationic protein (CAP18) with
lipopolygaccharide-inhibitory activity.";
Infect. Immun. 62:1421-1426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.; "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                            101838; Cathelicidin; 1.
172 AA; 19437 MW; 549EAC408DEB7A63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 135-159
    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SEQUENCE OF 135-159, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 179:170-175(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Bone marrow;
MEDLINE=91354246; PubMed=1883348;
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(TrEMBLrel.
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                                                                                                                                                                                    NCBI_TaxID=9615;
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P25230;
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CAP18 RAB
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes."; FRBS Lett. 370:46-52(1995).
-!- FUNCTION: CAP18 binds to the lipid a moiety of bacterial lipopolysaccharides (LPS), a glycolipid present in the outer membrane of all Gram-negative bacteria. Has antibiotic activity.
-!- TISSUE SPECIFICITY: Neutrophils.
-!- SIMILARITY: Belongs to the cathelicidin family.
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PDB; ILYP; NMR; @=135-166.

InterPro; IPR001094; Cathelicidin;

PANTHER; PTHR10206; Cathelicidin; 1.

PEODOM; PD001838; Cathelicidin; 1.

PROSTIE; PS00946; CATHELICIDINS 1; 1.

PROSTIE; PS00947; CATHELICIDINS 2; 1.

3D-structure; Antiblocit; Antimicrobial; Direct protein sequencing; Pyrrolidone carboxylic acid; Signal.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NWR OF 135-166.
MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8; Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-P., Huang T.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 FDISCDK--DNKRPALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTE 169
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Antimicrobial protein CAP7.
Pyrrolidone carboxylic acid (By similarity).
By similarity.
By similarity.
MEDLINE=94075827; PubMed=8254193;
Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D.,
Cavaillon J.-M., Warren H.S., Wright S.C.;
"A novel granulocyte-derived peptide with lipopolysaccharide-
neutralizing activity.";
J. Immunol. 152:231-240(1994).
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D7BF2103BCFB13C4 CRC64;
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107
157
171 AA;
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30
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                                                                                                                                                                                                                                                                                 TISSUE=Bone marrow;
MEDLINE=99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
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MEDLINE=98072398; PubMed=9409740; DOI=10.1016/S0014-5793(97)01310-0; Scocchi M.; Wang S., Zanetti M.; Scocchi M.; Wang S., Zanetti M.; Structural organization of the bovine cathelicidin gene family and identification of a novel member.";
                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=BWAP34;
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 457:459-464 (1999).

RMBL; AJ224929; CAA12228.1; -; mRNA.

RMSP; P23196; INWI.

SMR; O62842; 30-130.

GO; GO:00065276; C:extracellular region; IEA.

R GO; GO:0006513; P:response to pest, pathogen or parasite; IEA.

R GO; GO:000666; Cathelicidin.

R Fam; PF00066; Cathelicidins; 1.

R ProDom; PD001899; Cathelicidins; 1.

R PROSITE; PS00946; CATHELICIDINS 1; 1.

R PROSITE; PS00947; CATHELICIDINS 2; 1.
                                                                                                                                                                                                                                                                                                                         Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E., Zanetti M.; "Novel cathelicidins in horse leukocytes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myeloid cathelicidin 3.
5C35F1FA2D112BCB CRC64;
                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Myeloid cathelicidin 3 precursor.
Name=eCATH-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.0%; Score 457.5; DB 2
57.2%; Pred. No. 1.6e-35;
tive 24; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial peptide BWAP-34 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 AA; 19299 MW;
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                  O62842 HORSE PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                           Equus caballus (Horse).
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                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 95; Conserv
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NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>B</u>MA34 BOVIN
P56425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 LDPPPEQDVEHPGARKPVSFTVKETVCPRTTPQPPEQCDFKENGLVKQCVGTVTKYWIRG 119
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                   -1- FUNCTION: Exerts a potent antimicrobial activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKTORDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINORSSDANLYRLLD
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Probom; PD001838; Carhelicidin; 1.
PROSITE; PS00946; CATHELICIDINS_2; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
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Termen S., Tollin M., Olsson B., Svenberg T., Agerberth B.,
Gudmundsson G.H.;
Submitted (FRB-202) to the EMBL/GenBank/DDBJ databases.
EMBL, AF484553; AAQ05977.1; -; mRNA.
GO, GO:0005576; C:extracellular region; IRA.
GO, GO:0005952; P:defense response; IRA.
GO, GO:0009613; P:response to pest, pathogen or parasite; IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Potential.
Antibacterial peptide BMAP-34.
Pyrrolidone carboxylic acid.
Glycine amide (Potential).
By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 SPDISCDKDNKR--PALLGDFFRKSKEKIGKEFKRIVQRIKDFLR 162
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                                                                  and testis.
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Last annotation update)
                                                                                                                                                                                                                                                                               EMBL; Y12729; CAA73261.1; -; Genomic_DNA.
EMBL; Y12729; CAA73261.1; JOINED; Genomic_DNA.
EMBL; P31.96; 1KW1.
SMR; P56425; 30-129.
INTER: PTHR10206; Cathelicidin.
Pfam; PF00666; Cathelicidin; 1.
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Lett. 417:311-315(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.0*
Matches 99; Conservative
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NCBI_TaxID=10116;
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165 AA;
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NUCLEOTIDE SEQUENCE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                  65 PTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDIS 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Bone marrow;
MEDLINE-99402973; PubMed=10471829; DOI=10.1016/S0014-5793(99)01097-2;
Scocchi M., Bontempo D., Boscolo S., Tomasinsig L., Giulotto E.,
Zanetti M.;
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia, Butheria, Laurasiatheria, Perissodactyla, Equidae, Equus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R Wovel cathelicidine in horse leukocytes.";

R FEBS Lett. 457:459-464(1999).

R REMBL, AJ224927; CAA12226.1; -; mRNA.

R RSP; P32196; 1KWI.

R SPR; O62840; 30-130.

R GO; GO:0005576; C:extracellular region; IEA.

R GO; GO:0005513; P:cdefense response; IEA.

R GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.

R Ffam; PF00666; Cathelicidin; I.

R PROSITE; PS00194; CATHELICIDINS 1; I.

R PROSITE; PS00946; CATHELICIDINS 1; I.
                                                                                                                                                                                                                                                                                                                                                                                                                125 CDXDN-----KRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTE 169
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                                                                                                                                                                 DB 2; Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.3%; Score 451; DB 2; Length 156; 56.2%; Pred. No. 6e-35; ive 20; Mismatches 32; Indels
                                                                                                                                                                                                          48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 156 Potential.
156 AA; 17647 MW; BBBEA5D150288FFD CRC64;
                                                                                                  NON_TER 1 1 1 = SEQUENCE 171 AA; 19320 MW; 7E8F3DA9DF10E839 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Myeloid cathelicidin 1 precursor.
                                                                                                                                                               51.6%; Score 453.5; DB 2 55.6%; Pred. No. 3.8e-35;
                                                                                                                                                                                55.6%; Preu. ...
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                 Pfam, PP00666; Cathelicidins; 1.
ProDom, PD0019818; Cathelicidin; 1.
PROSITE, PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
InterPro, IPR001894; Cathelicidin.
                                                                                                                                                                                                        95; Conservative
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95, Conservative
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156
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                                                                                                                                                                                    Best Local Similarity
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MEDLINE=9525306, Pubmed=7737198;
MEDLINE=9525306, Pubmed=7737198;
TO881 A., Scocchi M., Zanetri M., Storici P., Gennaro R.;
PMAP-37, a novel antibacterial peptide from pig myeloid cells. CDNA cloning, chemical synthesis and activity.";
Bur. J. Biochem. 228:941-946(1995).
-!- FUNCTION: Exerts antimizationial activity against both Gram-positive and negative bacteria with minimal inhibitory concentrations ranging over 1-4 micro molar. Its activity appears to be mediated by its ability to damage bacterial membranes.
-!- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Antibacterial peptide PMAP-37 precursor (Myeloid antibacterial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                                                                                                                                                                                                                                                                                   Sus scrofa (Pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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PANTHER; PTHR10206; Cathelicidin; 1.
Prodom, PD001818; Cathelicidin; 1.
Prodom, PD001818; Cathelicidin; 1.
PROSITE; PS00946; CATHELICIDINS 1; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid; Signal.
121 PDISCDKON--KRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial peptide PMAP-37.
Pyrrolidone carboxylic acid (By
                                 120 FDVSCGEPQRVKRFG------MRILLPR
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                                                                                                                                                                                        167 AA
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By similarity.
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PIR; S68967; S68967.
                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                        STANDARD;
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130
167
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124
                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, 01-OCT-1996 (Rel. 34, 13-SEP-2005 (Rel. 48,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P32196; 1KWI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131
30
                                                                                                                                                                                                                                                                                                                                                                                Name=PMAP37;
                                                                                                                                                                                        PMP37 PIG
P49932;
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120 LDINCDEIQSVGRFRRLRKKTRKRLKKIGKVLKWI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19846 MW;
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                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130
173
176
30
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                                                                                                                                       Capra hircus (Goat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                    NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
174
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                        Lehrer R.I.;
                                                                               30-MAY-2000
                                                          CAPHI
                                                                                                       13-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPTIDE
PROPEP
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULPID
                                                                                                                                                                                                                                           Shamova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROPEP
                                   RESULT 13
  셤
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                                                                                                                                                                                                                                                                                                                                                                             This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LDQPPRADEDPGTPKPVSFTVKETVCPRPTWRPPELCDFKENGRVKQCVGTVTLNPSNDP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKTORDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
13.5EP-2005 (Rel. 48, Last amnotation update)
Antibacterial peptide PWAP-36 precursor (Myeloid antibacterial peptide
                                                                                                                                                                                                                                                            MEDLINE=94123775; PubMed=8293820; DOI=10.1016/0014-5793(94)80214-9; Storici P., Scocchi M., Tossi A., Gennaro R., Zanetti M.; Chemical synthesis and biological activity of a novel antibacterial peptide deduced from a pig myeloid cDNA."; PEBS Lett. 337:303-307(1994).

-! FUNCTION: Exerts antimicrobial activity against both Gram-positive and negative bacteria. Its activity appears to be mediated by its ability to damage bacterial membranes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSEP, P32196; 1KWI.
SMR; P49931; 30-130.
InterPro; IPRO1894; Cathelicidin.
PANTHER; PTH710206; Cathelicidin; 1.
ProDom; P000666; Cathelicidins; 1.
ProDom; P0004838; Cathelicidins; 1.
PROSITE; PS00946; CATHELICIDINS; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
Antibiotic; Antimicrobial; Pyrrolidome carboxylic acid; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial peptide PMAP-36.
Pyrrolidone carboxylic acid (By similarity).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Indels
           120 LDITCNEIQSVGLLSRLRDFLSDRGRRLGEKIERIGGKIKD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94B13C69709DA64B CRC64;
                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the cathelicidin family.
 121 FDISCDKDNK--RFALLGDFPRKSKEKIGKEFKRIVQRIKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 PDISCDKDNK--RPALLGDFFRKSKEKIGKEFKRI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.3%; Pred. No. 3.3e-34; ive 18; Mismatches 39
                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE, AND SYNTHESIS OF 130-166.
                                                                               166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.5%; Score 443.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Potential.
Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L29125; AAA31070.1; -; mRNA.
PIR; S41731; S41731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 AA; 18647 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95; Conservative
                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
                                                                                                                                                                                                                                                    TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                36).
Name=PMAP36;
Sus scrofa (Pig).
                                                                                                                                                                                                                    NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30
                                                                              PMP36 PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              removed.
                                                                                      P49931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD RES
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                       Ediaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE OF 131-149 AND 151-153, AND PROTEIN SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P32196; 1KWI.

SMR; P82018; 30-130.

InterPo. 1PR001894; Cathelicidin.

PANTHER, PTRR10206; Cathelicidin; 1.

Pfam; PF00666; Cathelicidin; 1.

ProDom; P0001838; Cathelicidin; 1.

PROSTTE; PS00946; CATHELICIDINS 1; 1.

PROSTTE; PS00947; CATHELICIDINS 2; 1.

PROSTTE; PS00947; CATHELICIDINS 2; 1.

PROSTTE; PS00947; CATHELICIDINS 2; 1.

PROSTOR Antibiotic; Antimicrobial; Direct protein sequencing; Pyrrolidone carboxylic acid; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proline amide (G-174 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ï
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                                                                                                                                                                                                                                                                                                                                                                                                                          O., Brogden K.A., Zhao C., Nguyen T., Kokryakov V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrrolidone carboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    group).
By similarity.
By similarity.
; 6PD7056C954E340A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- PTW: Blastase is responsible for its maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bactenecin 5.
Removed in mature form.
                                               (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 48, Last annotation update)
176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity)
                                                                                                                                  Bactenecin 5 precursor (Bac5) (ChBac5)
PRT;
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Bone marrow, and Leukocyte;
MEDLINE=99346202; PubMed=10417180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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us-10-815-562-2.rup

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MEDLINE-96440581; PubMed-8549789; DOI=10.1016/0014-5793(95)01390-3; Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.; "Molecular analysis of the sheep cathelin family reveals a novel antimicrobial peptide.", FEBS Lett. 377:519-522(1995).
                                                                                                                                                                                                   TISSUE-Liver;
A Huttner K.M., Mahoney M.M.;
A Huttner K.M., Mahoney M.M.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.

EMBL, U60597; AAB49712.1; -; Genomic_DNA.

R HSSP; P32196; IKWI.

R GO; GO:0006527; C:extracellular region; IEA.

R GO; GO:0006527; P:defense response; IEA.

R GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.

R GO; GC:0009665; Cathelicidin.

R ProDom; P000666; Cathelicidin.

R ProDom; P0001838; Cathelicidin.

R PROSITE; PS00946; CATHELICIDINS 1.

R PROSITE; PS00947; CATHELICIDINS 2; 1.

S EQUENCE 165 AA; 18827 MW; F043047B3728A9CD CRC64;
                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
  TISSUE=Liver;
g
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                           60 LDPAPNDEVDPGTRKPVSFTVKETVCPRTTQQPPERCDFKENGLVKQCVGTVTLDPSNDQ 119
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  61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKTORDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Purification and properties of proline-rich antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Capra hirus (Goat).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

Pecora; Bovidae; Caprinae; Capra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 50.3%; Score 442.5; DB 2; Length Local Similarity 68.5%; Pred. No. 4.5e-34; nes 87; Conservative 19; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y18873; CAC80206.1; -; mRNA.
SEQUENCE 176 AA; 19846 MW; 6FD7056C954E340A CRC64;
                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                         176 AA
                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Bone marrow;
MEDLINE=99346202; Pubmed=10417180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from sheep and goat leukocytes.";
Infect. Immun. 67:4106-4111(1999)
                                                                                                                                                                                                                                                                                                                                     13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, Bac5 protein.
                                                                                                                                                                                                                                                                      04JFB9 CAPHI PRELIMINARY;
Q4JFB9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:|::
FDINCNE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDISCDK 127
                                                                                                       PDISCDK 127
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|20 FDINCNE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lehrer R.I.;
                                                                                                       121
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P79360 SHE
D P7936
AC P7936
DT 01-MA
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Ovis aries (Sheep). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Caprinae, Ovis.

NUCLEOTIDE SEQUENCE

NCBI_TaxID=9940;

P79360_SHEEP PRELIMINARY; PRT; 165 AA.
P93360;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
Myelold antimicrobial peptide.
Name-Map-34;

SHEEP

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61 LDPRPTMDG-DPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARG 119
                                                                                                                                                     60 LDPPPEQDAEDRGARKPVSFKVKETVCPRTSQQPVEQCDFRKNGLVKQCVGTVTRYWIRG 119
                                                                          9
                                                                                                      59
                                                                                         1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
                                               Gaps
                                             . 9
                                                                                                                                                                                                               120 SPDISCDKDNKRFALLG---DFFRKSKEKIGKEFKRIVQRIXDFLR 162
               Length 165;
                                             42; Indels
              50.1%; Score 440; DB 2;
57.8%; Pred. No. 7.2e-34;
ive 22; Mismatches 42;
                                                                                                                                                                                                                                                                        Search completed: January 12, 2006, 21:50:32
Job time : 84.8044 secs
```

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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100.0%; Score 879; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.1e-95;
Matches 170; Conservative 0; Mismatches 0;
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TOPOLOGY: linear
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Sequence 7862, Ap
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1 MKTQRDGHSLGRWSLVLLLL......KRIVQRIKDFLRNLVPRTES 170
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/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-09-312-911-2
US-09-917-340-32
US-09-313-9992-7862
US-09-313-911-4
US-09-317-340-33
US-09-917-340-34
US-09-917-340-34
US-09-917-340-34
US-09-917-340-34
US-09-128-345-4
US-08-243-879A-36
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Maximum Match 100%
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Match Length
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No.
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Sequence 2, Application US/08313681A
; Sequence 2, Application US/08313681A
; Patent No. 5618675
; GENERAL INFORMATION:
APPLICANT: Wight, Sueme W.
APPLICANT: Wight, Sueme C.
APPLICANT: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STRATE: California
                                                                 Sequence 5, Appli
Sequence 1180, Ap
Sequence 17, Appl
Sequence 10, Appli
Sequence 6, Appli
Sequence 11, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appli
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                                           4349, Ap
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
PILLING DATE:
US-09-385-328-8

US-09-917-340-36

US-09-917-340-28

US-09-513-990C-4349

US-08-313-681A-5

US-09-322-911-5

US-09-385-328-10

US-09-385-328-10

US-09-385-328-11

US-09-385-328-11

US-09-325-916-6

US-09-325-916-6

US-09-325-916-6

US-09-325-916-6

US-09-325-916-8

US-09-276-202-8

US-09-276-202-8

US-09-276-202-10

US-09-276-202-10

US-09-276-202-10

US-09-276-202-10
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CLALING LALES:
CLALING LALES:
CLALING LALES:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELEPHONE: 415-326-2400
TELEPHONE: 415-326-2402
TELEPHONE: 415-326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
    415.5
410.5
410.5
333
325
325
314
203.5
197.5
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9 9

Gaps

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Length 170; Indele 120

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Sequence 7862, Application US/09513999C
; Sequence 7862, Application US/09513999C
; Reneral Information
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; APPLICANT: Duclert, A.
; TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR PILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFFWARE: Patent.pm
                                                                                                                            61 LDPRPTWDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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                                                                                                                                                                                                                                 Query Match 99.4%; Score 874; DB 2; Length 170; Best Local Similarity 99.4%; Pred. No. 4.3e-95; Matches 169; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/0991340

Sequence 32, Application US/0991340

Patent No. 6696238

GENERAL INFORMATION:

APPLICANT: Murphy, Christopher J.

APPLICANT: Machulty, Jonathan F.

APPLICANT: Reid, Ted W.

TITLE REFERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: US/09/917,340

CURRENT FILING DATE: 2000-07-29

PRIOR APPLICATION NUMBER: 60/221,632

PRIOR FILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/249,602

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 3:

LENGTH: 170
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CORGANISM: Homo sapiens
US-09-917-340-32
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US-09-513-999C-7862
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                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: TWO Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                 61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                           61 LDPRPTMDGDPDTPKPVSFTVKETYCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15325-000920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/691,280
FILLING DAYE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILLING DAYE: JULY 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILLING DAYE: JULY 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILLING DAYE: JULY 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILLING DAYE: SEPTEMBER: 77, 1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
REGISTRATION NUMBER: 35,136
TELEPHONE: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-322-911-2
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GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Larrick, Susan C.
APPLICANT: Hista, Mishimse
APPLICANT: Hista, Mishimse
APPLICANT: Balint, Robert P.
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                          61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                  60 MDPQQLEDAKPYTPQPVSPTVKETECPRTTWKLPEQCDFKEDGLVKRCVGTVTRYQAWDS 119
                                                                            1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKBAVLRAIDGINQRSSDANLYRLLD
       Gape
                                                                                                                                                                                                                                   121 FDISCDK--DNKRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPRTE 169
                                                                                                                                                                                                                                                             3,
    44; Indels
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COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/09/322,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSER: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
    26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION NUMBER: 07/916,765
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: 08/913,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09322911
Patent No. 6103888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 171 amino acids TYPE: amino acid
    98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
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    Matches
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Sequence 4, Application US/08313681A

Patent No. 5618675

GENERAL INFORMATION:
APPLICANT: Wright, James W.
APPLICANT: Wright, Suan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
CORRESPONDENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEB: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Prancisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFXKDGLVKRCMGTVTLNQARGS 120
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                                                                                                                                                                                                                                                                                                                                                                            4 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 63
                                                                                                                                                                                                                                                                                                                                                 1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINORSSDANLYRLLD
                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                         Length 152
                                                                                                                                                                                                                                                                                                    1; Indels
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ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
                                                                                                                                                                                                                                                    86.6%; Score 761; DB 2;
98.6%; Pred. No. 8.2e-82;
ilve 1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PDISCDKDNKRPALLGDFFRKSKEKIGK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:

NAME/KRY: SIGNAL

LOCATION: -33..-1

CTHER INFORMATION: SEQ LLIGLUMPLAIIA/QV
US-09-513-999C-7862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFRENCE/DOCKET NUMBER: 1532;
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.0%;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 171 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.64
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-313-681A-4
                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
SEQ ID NO 7862
LENGTH: 152
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US-08-313-691A-4
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120 NFDITC 125
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US-09-917-340-34
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                                                                                                                                                                 LENGTH: 156
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                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                   61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKXDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDPKKCCGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 LDPLFKGDKDSDTPKPVSFMVKETVCPRIMKQTPEQCDFKENGLVKQCVGTVILDPVKDY 119
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                                                                                1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLD 60
                                                                                                       Gaps
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                                                                                                                                                                                                                                                                         3
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    Length 171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 53.0%; Score 465.5; DB 2; Length 3 Similarity 57.3%; Pred. No. 8e-47; 98; Conservative 26; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 US-09-917340-340-39, Application US/09917340
| Patent No. 6696238
| GENERAL INFORMATION:
| APPLICANT: Murphy, Christopher J.
| APPLICANT: McAnulty, Jonathan F.
| APPLICANT: McAnulty, Jonathan F.
| APPLICANT: Reid, Ted W.
| TITLE OF INVENTION: Transplant Media FILE REFERENCE: TPLANT-06468
| CURRENT APPLICATION NUMBER: US/09/917,340
| CURRENT FILING DATE: 2001-07-28
| PRIOR APPLICATION NUMBER: 60/221,632
| PRIOR PILING DATE: 2000-01-17
| PRIOR PILING DATE: 2000-01-17
| PRIOR PILING DATE: 2001-05-15
| NUMBER OF SEQ ID NOS: 96
| SOFTWARE: PATENT ON ON S: 200
| SOFTWARE: PATENT ON ON S: 200
| SERIOR OF SEQ ID NOS: 96
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Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REPERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.2%
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Equus caballus
US-09-917-340-33
Query Match
Best Local Similarity
Matches 98, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-917-340-35
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61 LDPRPIMDGD-PDIPKPVSFTVKETVCPRITQQSPEDCDFKKDGLVKRCMGTVTLNQARG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 LDPLPKGDKDSDTPKPVSFMVKETVCPRIMKQTPEQCDFKENGLVKQCVGTVILGPVKDH 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKTORDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 FDISCDKON--KRFALLGDFFRKSKEKIGKEFKRIVQRIKDFLRNLVPR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 51.3%; Score 451; DB 2; Length 156; Best Local Similarity 56.2%; Pred. No. 3.6e-45; Matches 95; Conservative 20; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch
1 Similarity 67.5%; Pred. No. 6.5e-43;
85; Conservative 19; Mismatches 20; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOS-09-91. Application US/09917340
Fatent No. 669628
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Methulty, Jonathan F.
APPLICANT: Methulty, Jonathan F.
TITLE OF INVENTION: Transplant Media
FITLE OF INVENTION: Transplant Media
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT APPLICATION NUMBER: 60/221,632
FRIOR APPLICATION NUMBER: 60/221,632
FRIOR APPLICATION NUMBER: 60/290,932
FRIOR FILING DATE: 2000-01-17
FRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 34
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                              ; ORGANISM: Equus asinus US-09-917-340-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 85; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 SFDISC 125
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURABILGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 2000
TELECOMMUNICATION:
                 TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
(202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                               83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 65.4
Matches 83; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acide
                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 PDISCDK 127
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| 120 LDITCNE 126
                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
  TELEPHONE:
                                                                                                                                                                                      US-08-243-879A-38
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                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 LDQPPQDDEDPDSPKRVSFRVKETVCSRTTQQPPEQCDFKENGLLKRCEGTVTLDQVRGN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.6%; Score 427.5; DB 2; Length 155; 66.7%; Pred. No. 2.1e-42; tive 18; Mismatches 23; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-243-879A-38

i Sequence 38, Application US/08243879A

i Patent No. 5708145

i GENERAL INFORMATION:
APPLICANT: LEBRER R. ROBERT I.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500

CITY: Washington, DC

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAX-1994
                               US-09-917-340-29

Sequence 29, Application US/09917340

Sequence 29, Application US/09917340

Sequence 29, Application US/09917340

GENERAL INVORMATION:
APPLICANT: MacAnily, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REPERENCE: TPLANT-06468

CURRENT APPLICATION NUMBER: US/09/917,340

CURRENT FILING DATE: 2001-07-29

FRIOR APPLICATION NUMBER: 60/221,632

FRIOR PRILING DATE: 2000-11-17

FRIOR PILING DATE: 2000-11-17

FRIOR FILING DATE: 2000-11-17

FRIOR FILING DATE: 2000-11-17

FRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 96

SOFTWARE: PATCHTING DATE: 2010-05-15

NUMBER OF SEQ ID NOS: 96

SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2000-0540.22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7%
Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bos taurus
US-09-917-340-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDISCD 126
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FDITCN 125
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61 LDPRPTMDGDPDTPKPVSPTVKRTVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                                                                                                                                                                                       60 LDQPPKADEDPGTPKPVSPTVKETVCPRPTRQPPELCDFKENGRVKQCVGTVTLDQ1KDP 119
                                                                                                                                          1 MKTQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLD
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47.6%; Score 418.5; DB 1; Length 147; 65.4%; Pred. No. 2.3e-41;
                                                   19; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08499523
Sequence 4, Application US/08499523
Setent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: ROKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITT: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-UUL-1995
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US-08-243-879A-36
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                                                                  61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
                                                                                    60 LDQPPKADEDPGTPKPVSFTVKBTVCPRPTRQPPELCDFKENGRVKQCVGTVTLDQIKDP 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONDITY: USA
CONDITY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-MG-1998
CLASSIFICATION NUMBER: US/09/128,345
FLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMM: COPILEZ, LAURA, 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELEFROMINICATION INFORMATION:
TELEFROM: (212) 790-9090
TELEFROM: (212) 790-9090
TELEFROM: (212) 790-9090
TELEFROM: (212) 790-9090
TELEFROM: GLAIP PENNE:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TENDER: 664-1 PENNE:
LENGTH: 147 amino acids
                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                   121 PDISCDK 127
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61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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; Sequence 40, Application US/08243879A
; Patent No. 2708145
; GENERAL INFORMATION:
    APPLICANT: LEHRER, ROBERT I.
; TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CCITY: Washingron, DC
CCINTY: Washingron, DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
                                                                                                                                                                                                                                         COUNTRY: WEALINGSON, DC.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUW TYPE: FIDEPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISCOMMUNICATION INFORMATION:
TELEPROMOTICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 887-0763
TELEREAX: (202) 887-0763
TELEREAT SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PDISCDK 127
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Query Match 47.6%; Score 418.5; DB 1; Length 149;
Best Local Similarity 65.4%; Pred. No. 2.3e-41;
Matches 83; Conservative 19; Mismatches 24; Indels 1; Gaps
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
CLASSIFCATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MURABAHIGE, KATE H.
REGISTRAATION NUMBER: 2000-0540.22
TELEFROMONICATION INFORMATION:
TELEFROMONICATION INFORMATION:
TELEFROM: (202) 887-1500
TELEFROM: (202) 887-1500
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: APPRICATED:
US-08-243-879A-40
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Search completed: January 12, 2006, 21:51:59 Job time : 26.3469 secs

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38, Appl
38, Appl
38, Appl
39, Appl
34, Appl
34, Appl
34, Appl
                                                            January 12, 2006, 21:45:40 ; Search time 70.2583 Seconds (without alignments) 1010.998 Million cell updates/sec
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1 MKTQRDGHSLGRWSLVILLL......KRIVQRIKDFLRNLVPRTES 170
                                                                                                                                                                                                                                                                                                                                                                                                                Description
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Sequence 3
Sequence 3
Sequence 5
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Sequence 1
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                                                                                                                                                                                                                                                                     Published Applications AA Main:*

'Ggn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

'Ggn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

'Ggn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

'Ggn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

'Ggn2_6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

'Ggn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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US-10-893-485-51
US-10-910-139-40
US-10-910-119-47
US-10-910-119-47
US-10-87-436A-513
US-10-287-436A-513
US-10-344-709C-11
US-10-344-709C-7
US-10-844-837-33
US-10-909-119-48
US-10-909-119-50
US-10-919-119-49
US-10-919-119-49
US-10-944-837-34
US-10-944-837-34
US-10-99-917-340-34
US-10-99-917-340-34
US-10-944-837-34
US-10-99-917-340-29
US-10-344-709C-5
US-10-344-709C-5
US-10-344-709C-5
US-10-344-709C-5
US-10-344-709C-5
US-10-344-709C-5
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                1867569 seqs, 417829326 residues
                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                             OM protein
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                                                                                                                       Sequence:
                                                               Run on:
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Sequence 51, Application US/10603566

Sequence 51, Application US/10603566

Bublication No. US20040086966A1

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Communi, David
APPLICANT:
Communi, David
APPLICANT:
APPLICANT:
APPLICANT:
Communi, David
APPLICANT:
APPLICANTON NUMBER:
US 60/303,858
FRIOR PILING DATE: 2001-07-13
FRIOR APPLICATION NUMBER:
BRIOR APPLICATION NUMBER:
APPLICANTON NUMBER:
APPLI
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              Sequence Seq
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US-10-909-119-44
US-10-657-851-29
US-09-539-443-4
US-09-539-443-6
US-09-539-443-10
US-09-539-443-10
US-09-539-443-10
US-00-627-829-6
US-10-627-829-6
US-10-627-829-6
US-10-627-829-6
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US-10-627-829-10
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US-10-893-485-51
Squarence 51, Application US/10893485
Publication No. US/0050155090A1
GENERAL INFORMATION:
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; LENGTH: 170
; TYPE: PRT
: ORGANISM: Homo sapiens
US-10-603-566-51
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Sequence 4, Application US/10777683; Publication No. US2050032117A1; GENERAL INFORMATION: APPLICANT: Richard B. Moss
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CRGANISM: Homo sapiens
US-10-844-837-32
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                     APPLICANT: Community, Dayler Ann APPLICANT: Vandenbogaerde, Ann APPLICANT: Detheax, Michel APPLICANT: Parmentier, Marc CURRENT APPLICANTION: Compositions and Methods Comprising a Ligand of ChemerinR; TILE OF INVERNIT APPLICATION NUMBER: US 10/893,485 CURRENT PILING DATE: 2004-07-16 PRIOR PILING DATE: 2004-07-09 PRIOR PILING DATE: 2001-07-09 PRIOR PILING DATE: 2001-07-13 PRIOR APPLICATION NUMBER: US 09/905,253 PRIOR PILING DATE: 2001-07-13 PRIOR PILING DATE: 2001-07-13 PRIOR PILING DATE: 2001-07-23 NUMBER OF SEQ ID NOS: 97 SEQ I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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99.4%; Pred. No. 5.9e-87;
tive 1; Mismatches 0; Indels
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| Batent No. US20020090369A1
| GENERAL INFORMATION:
| APPLICANT: Wurphy, Christopher J.
| APPLICANT: Warnulty, Jonathan F.
| APPLICANT: Reid, Ted W.
| TILLE OF INVENTION: Transplant Media FILE REFERENCE: TPLANT-06468
| CURRENT APPLICATION NUMBER: US/09/917,340 CURRENT FILING DATE: 2001-07-29
| PRIOR APPLICATION NUMBER: 60/221,632 PRIOR PILING DATE: 2000-07-28
| PRIOR PILING DATE: 2000-11-17
| PRIOR PILING DATE: 2001-01-17
| PRIOR PILING DATE: 2001-05-15
| PRIOR PILING DATE: 2001-05-15
| NUMBER OF SEC ID NOS: 96
| SOFTWARE: Patentin Ver: 2.0
Wittamer, Valerie
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Best Local Similarity 99.4
Matches 169; Conservative
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; ORGANISM: Homo sapiens
US-10-893-485-51
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ORGANISM: Homo sapiens
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61 LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGS 120
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APPLICANT: Teruo Kirikae
TITLE OP INVENTION: Method for Assessment of Cystic Lung Fibrosis
FILE REFERENCE: 074236
CURRENT APPLICATION NUMBER: US/10/777,683
CURRENT PILING DATE: 2004-02-13
PRIOR APPLICATION NUMBER: US 60/447,310
PRIOR FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                121 PDISCDKDNKRPALLGDFPRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 170
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US-10-844-837-32
Sequence 32, Application US/10844837
Sequence 32, Application US/10844837
Sequence 32, Application US/10844837
Sequence 32, Application US/10844837
GENERAL INFORMATION: Michael
APPLICANT: Homan, Jane
TITLE OF INVENTION: Targeted Biocides
FITLE REFERENCE: IOGEN-09014
CURRENT APPLICATION NUMBER: US/10/844,837
CURRENT PILIG DATE: 2004-05-13
NUMBER OF SEQ ID NOS: 101
SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
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Query Match
Best Local Similarity 99.4
Matches 169; Conservative
                                       TYPE: PRT; ORGANISM: Homo sapiens
US-10-657-851-32
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US-10-287-436A-1204
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SEQ ID NO 32
LENGTH: 170
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Publication No. US20050079578A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Centanni, John M.
APPLICANT: Allen-Hoffmann, Lynn
TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
TITLE REPERENCE: STRAIA-0710
CURRENT APPLICATION NUMBER: US/10/909,119
CURRENT FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 128
SCOTWARE: Patentin version 3.2
SEQ ID NO 47.
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99.4%; Score 874; DB 5; Length 170;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0; Indels
    0; Indels
  1; Mismatches
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Fublication No. US20050089836A1
GENERAL INPORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: Machalty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE REPERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/10/657,851
CURRENT FILING DATE: 2003-09-09
FRIOR PILING DATE: 2000-07-29
FRIOR PILING DATE: 2000-07-28
FRIOR FILING DATE: 2000-01-8
FRIOR APPLICATION NUMBER: 60/221,632
FRIOR FILING DATE: 2000-01-17
FRIOR FILING DATE: 2000-01-17
FRIOR FILING DATE: 2000-01-17
FRIOR FILING DATE: 2000-01-17
FRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATENT VET. 2001-05-15
    169; Conservative
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ORGANISM: Homo sapiens
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LDPRPTMDGDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKUDGLVKRCMGTVTLNQARGS 120
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      Length 170;
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TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
FILLE OF INVENTION: RECENTED ARTHRITIS
FILLE REFERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT APPLICATION NUMBER: US/05.10-31
FRIOR APPLICATION NUMBER: US 60/336,220
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Publication No. US20050202421A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAT: CHILDREN'S HOSPITAL MEDICAL CENTER
TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: RHEUMATOID ARTHRITIS
FILE REFERENCE: 10872.514696
CURRENT APPLICATION NUMBER: US/10/287,436A
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/336,220
Score 874; DB 5;
Pred. No. 5.9e-87;
1; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 513
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-287-436A-513
Sequence 513, Application US/10287436A
Publication No. US20050202421A1
GENERAL INFORMATION:
      99.4%;
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TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: Vaccine which comprises at least one antigen and a cathelicidin TITLE OF INVENTION: derived antimicrobial peptide or a derivative thereof FILE REFERENCE: SONN **1300S**

CURRENT PEDILICATION NUMBER: US/10/344,709C

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: PCT/EP01/09529

PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 52.0%; Score 457.5; DB 3; Length 170; 1 Similarity 57.2%; Pred. No. 1.8e-41; 95; Conservative 24; Mismatches 38; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-344-709C-7
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APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE CANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT FILING DATE: 2001-07-29
PRIOR RILING DATE: 2000-07-28
PRIOR RILING DATE: 2000-01-39
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-15
PRIOR FILING DATE: 2001-01-15
SPIOR FILING DATE: 2001-05-15
FRIOR FILING DATE: 2001-05-15
FRIOR FILING DATE: 2001-05-15
FRIOR FILING DATE: 2001-05-15
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Patent No. US20020090369A1
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ORGANISM: Artificial Sequence
       APPLICANT: JORG FRITZ ET AL.
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Matches 95;
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Bublication No. US20040170642A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: SONN:0300S

CURRENT PAPLICATION NUMBER: DC/10/344,709C

CURRENT PAPLICATION NUMBER: DC/10/344,709C

CURRENT PAPLICATION NUMBER: DC/FP01/09529

PRIOR APPLICATION NUMBER: DC/FP01/09529

PRIOR FILING DATE: 2000-08-17

PRIOR FILING DATE: 2000-08-17

SOFTWARE PAPLICATION NUMBER: A 1416/2000

PRIOR FILING DATE: 2000-08-17

SOFTWARE: PAPLICATION NUMBER: A 1416/2000

BRIOR PILING DATE: 2000-08-17

SOFTWARE: PALENTH: 170

LENGTH: 170
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                                                                                                                                                                                                                                       Length 170;
                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                  Query Match
99.4%; Score 874; DB 5;
Best Local Similarity 99.4%; Pred. No. 5.9e-87;
Matches 169; Conservative 1; Mismatches 0
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 1446
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1204
LENGTH: 170
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                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                  US-10-287-436A-1204
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60 LDPLPKGDXDSDTPKPVSFMVKETVCPRIMKQTPEQCDFKENGLVKQCVGTVILDPVKDY 119
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APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Feld, Ted W.
TILLB OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
PRIOR PILING DATE: 2003-09-09
PRIOR FILING DATE: 2000-07-29
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 33
LENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: January 12, 2006, 21:54:02
Job time : 71.2583 secs
                                                                                                                                                                                                  Sequence 33, Application US/10657851; Publication No. US20050089836A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Equus caballus
US-10-657-851-33
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Fublication No. US20050079578A1
GENERAL INFORMATION:
APPLICANT: Centenni, John M.
APPLICANT: Centenni, Lyun
TITLE OF INVENTION: Human Skin Equivalents Expressing Exogenous Polypeptides
FILE REFERENCE: STRAIA-09123
CURRENT APPLICATION NUMBER: US/10/909,119
CURRENT FILING DATE: 2004-07-30
NUMBER OF SEQ ID NOS: 128
SOFTWARE: Patentin version 3.2.
SEQ ID NO 48
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  LDPLPKGDKDSDTPKPVSFMVKGTVCPRIMKQTPEQCDFKENGLVKQCVGTVILDPVKDY 119
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                                              FDISCDKON--KRFALLGDFFRKSKEKIGKBFK-----RIVQRIK 158
                                                                         120 FDASCDEPQRVKRFHSVGSLIQRHQQMIRDKSBATRHGIRIITRPK 165
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                                                                                                                                                                        Sequence 33, Application US/10844837
; Publication No. US20050014932A1
; GENERAL INFORMATION:
APPLICANT: Imboden, Michael
; APPLICANT: Imboden, Michael
; APPLICANT: Bremel, Robert D.
TITLE OF INVENTION: Targeted Blocides
FILE REFERENCE: IOGEN-09014
; CURRENT APPLICATION NUMBER: US/10/844,837
; CURRENT FILING DATE: 2004-05-13
; NUMBER OF SEQ ID NOS: 101
; SOOTWARE: PatentIn version 3.2
; SEQ ID NO 33
...ERGTH: 170
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Matches 95, Conservative
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US-10-844-837-33
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ORGANISM: Equus caballus
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61 LDPRPTMDGDPDTPKPVSPTVKBTVCPRTTQQSPBDCDFKKDGLVKRCMGTVTLNQARGS 120
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121 PDISCDKDN--KRPALLGDFPRKSKEKIGKEFK-----RIVQRIK 158
                       121 PDISCDKDN--KRFALLGDFFRKSKBKIGKBFK-----RIVQRIK 158
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134 LLGDPFRKSKEKIGKEFKRIVQRIKDFLRNLVPRIES 170
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Sequence 1409, Ap
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Sequence 2, Appl
Sequence 9, Appl
Sequence 198, Appl
Sequence 198, Appl
Sequence 254, Appl
Sequence 347, Appl
Sequence 348, Appl
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Sequence 2104, Ap
Sequence 20, Appl
Sequence 6, Appli
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1990, Ap
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                                                                                                              January 12, 2006, 21:48:15; Search time 7.52768 Seconds (without alignments) 213.508 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-10-793-626-406
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US-11-196-475-68
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US-11-192-967-2
US-11-193-715-2
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Sequence 196, App
Sequence 199, App
Sequence 2, Appli
Sequence 19, Appl
Sequence 25, Appl
Sequence 21, Appl
Sequence 24, Appl
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              Sequence 1013, Ap Sequence 8036, Ap Sequence 964, App Sequence 1283, App Sequence 1016, Ap Sequence 1016, Ap Sequence 160, App Sequence 159, App Sequence 159, App Sequence 197, App Sequence 1, App Sequenc
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NUMBER OF SEQ ID NOS: 29
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 37
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Publication No. US2005025606941

GERERAL INFORMATION:

APPLICANT: Manoharan, Wuthiah
APPLICANT: Rajeev, Kallanthottathil G.

TITLE OF INVENTION INVA AGENTS WITH BIOCLEAVABLE TETHERS
ITLE REPERENCE: 14174-099016

CURRENT APPLICATION NUMBER: US/10/985,426

CURRENT PILING DATE: 2004-11-09

PRIOR PLILING DATE: 2004-08-10

PRIOR PLILING DATE: 2004-04-16

PRIOR PLILING DATE: 2003-04-25

PRIOR PLILOR DATE: 2003-08-11

PRIOR PLILOR DATE: 2003-08-11

PRIOR PLILOR DATE: 2003-08-15

PRIOR PLILOR DATE: 2003-09-15

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21.0%; Score 185; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.2e-14;
Matches 37; Conservative 0; Mismatches 0; Indels
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US-10-821-234-1013

US-10-467-657-8036

US-11-186-284-33

US-11-186-284-33

US-10-995-561-1016

US-10-995-561-1016

US-11-033-365-150

US-11-033-365-196

US-11-033-365-196

US-11-033-365-197

US-11-033-365-196

US-11-033-365-196

US-11-033-365-196

US-11-033-365-196

US-11-033-365-196

US-11-033-365-196

US-11-033-365-196

US-11-033-365-196

US-11-00-183-196

US-11-00-1
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ORGANISM: Artificial Sequence
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63 PRPIMDGDPDTPKPVSFIVKETVCPRITQQSPEDCDFKKDGLVKRCMGIVTLNQARGSFD 122
                                                                                                                                                                                                                                                                                 Sequence 20, Application US/10131826A
Publication No. US20050245730A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/049911
PRIOR PILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watanabe, Colin K
Wood, William
                                                                                                                                                                                                                                                                                                                                                                            Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gao, Wei-Qiang
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Godowski, Paul J. Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherwood, Steven
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumas, Daniel
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 YYKKQSSDKLTQSAIDGMVKELKDPYSEYMTAEETKQFNEGVSGDFVG-----IG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 WSLVLLLLGLVMPLAIIAQV----LSYKEAVLRAIDGINQRSSDANL----YRLLDLD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 WHFILVILGIILLTSIITVVSTILISHQKS-----GLN-KEQRANLKKIEYVYQTLNKD 84
                                                                                                                                                                            APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILLE REFERENCE: PU348002
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE PACENTIN Ver: 2.1
SSOFTWARE PACENTIN Ver: 2.1
SSOFTWARE PACENTIN Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2104, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION NO. US20050255478A1
GENERAL INFORMATION NO. US20050255478A1
APPLICANT: KIMMERLY, MILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUB480018
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PILICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
EENGTH: 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Сарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: amino acid sequence
US-10-793-626-406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: synthetic;
OTHER INFORMATION: amino acid sequence
US-10-793-626-2104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.7%; Score 76.5; DB 6; Length 491; Best Local Similarity 21.3%; Pred. No. 0.91; Matches 33; Conservative 30; Mismatches 65; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.7%; Score 76.5; DB 6; Length 491;
21.3%; Pred. No. 0.91;
tive 30; Mismatches 65; Indels 2
  LLGDFPRKSKEKIGKEFKRIVQRIKDFLRNLVPRTES 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 ISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRI 157
                                                                                        US-10-793-626-406

"Sequence 406, Application US/10793626

"Publication No. US20050255478A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 33; Conserva
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PRIOR PILLING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-17
PRIOR PILLING DATE: 1997-09-17
PRIOR PILLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILLING DATE: 1997-09-17
PRIOR PILLING DATE: 1997-09-18
PRIOR PILLING DATE: 1997-09-18
PRIOR PILLING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR PILLING DATE: 1997-09-19
PRIOR PILLING DATE: 1997-09-19
PRIOR PILLING DATE: 1997-09-19
PRIOR PILLING DATE: 1997-09-19
PRIOR SPILLING DATE: 1997-09-19
PRIOR PILLING DATE: 1997-09-19
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R.12310R.121,826A
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
85 YYKKQSSDKLİQSAIDGMVKELKDPYSEYMTAEFIKQFNEGVSGDFVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.0%; Score 70.5; DB 6; Length 867; 20.4%; Pred. No. 9.1;
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                                                                                                                                                                          135 AEMQKKNEQISVTSPMKDSPAEKAGIQPKDIVTQV 169
                                                                                               123 ISCDKDNKRFALLGDFFRKSKEKIGKEFKRIVQRI 157
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                           ---- BTVCPRTTQ---QSPEDCDFXKDGLVKRCMGTVT 113
                                                                                                                      425 NDKVDAQEENFLPKYQRVKDLCQRABYQTACEQLGQKWQCVEDATGKLK--LHKCKGPMR 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 TADHGYHIGQFGLV---KGKSMPYEFDIRVPFY-----VRGPNVEAGCLNPHIVLNID 364
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  ----SFTVK----- 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                     114 INQAR------GSFDISCDXDNKRFALLGDFFRKSKEKIGKEFK 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.0%; Score 70.5; DB 6; Length 870; Best Local Similarity 20.4%; Pred. No. 9.1; Matches 47; Conservative 27; Mismatches 59; Indels 9
                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10933025
; Sequence 6, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN
; APPLICANT: TOMITA, MEGUMI
; TITLE OF INVENTION: SULfotransferases and methods of use;
; TITLE OF INVENTION: thereof
; TITLE OF INVENTION: thereof
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: 10/025,966
; PRIOR APPLICATION NUMBER: 60/259,77
; PRIOR PILING DATE: 2001-12-27
; PRIOR PILING DATE: 2001-12-27
; PRIOR FILING DATE: 2001-12-27
; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NOS: 26
; SEQ ID NOS: 26
; SEQ ID NOS: 26
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Sequence 15, Application US/10933025
Sequence 15, Application US/10933025
Publication No. US20050265987A1
GENERAL INFORMATION:
APPLICANT: ROSEN, STEVEN
APPLICANT: HEMMERICH, STEFAN
APPLICANT: TOWAITA, MEGUMI
TITLE OF INVENTION: Sulfotransferases and methods of use;
TITLE OF INVENTION: thereof;
FILE REPERENCE: UCAL-230CON
CURRENT APPLICATION NUMBER: US/10/933,025
63 PRPT------MDGDP----DTPKPV--
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                    RESULT 5
US-10-933-025-6
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Sequence 1409, Application US/10821234

Sequence 1409, Application US/10821234

Publication No. US20050255114A1

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Adarmani, Susan
APPLICANT: Andarmani, Susan
APPLICANT: Annoy Y. Tom
ITILE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT PILING DATE: 2004-04-07

PRIOR APPLICANION NUMBER: US 60/462,047

PRIOR PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SEQ ID NO 1409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | : | | : | | : | | 425 NDKVDAQEENFLPKYQRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLK--LHKCKGPMR 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 KPVSFTVKETVCPRTTQQSPEDCDFKKDGL-VKRCMGTVTLNQARGSFD-ISCDKDNKRP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TQRDGHSLGRWSLVLLLLGLVMPLAIIAQVLSYKRAVLRAIDGINQRSSDANLYRLLDLD 62
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483 LGGSRALSNLVPKYYGQGSBACTCDSGDYKLSLAG----RRKKLFKKYK 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Indels 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.0%; Score 70.5; DB 6; Length 870; Best Local Similarity 20.4%; Pred. No. 9.1; Matches 47; Conservative 27; Mismatches 59; Indels 9
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8.0%; Score 70; DB 6
Best Local Similarity 24.0%; Pred. No. 6.8;
Matches 36; Conservative 22; Mismatches
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CURRENT FILING DATE: 2004-09-01
PRIOR PILING DATE: 2001-12-1
PRIOR FILING DATE: 2001-12-21
PRIOR PILING DATE: 2001-12-21
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/267,831
PRIOR FILING DATE: 2001-09-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PASLESQ for Windows Version 4.0
SOFTWARE: 970
                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1409
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73 TPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKDNKRF 132
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118 RONEADGGWSLVITGRQDYETATMGSYVFSIQVEGESQAVLVALEIVN------- 165
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                                                                                                                                                                                       13 WSLVLLLIGLVMPLAIIAQVLSYKEAVLRAIDGINQRSSDANLYRLLDLDPRPTMDGDPD
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APPLICANT: Mathls, John P.
APPLICANT: Mathls, John P.
TYLIE CANTI Meyer, Terry B.
TITLE OF INVENTION: Lepidopteran Insects and Methods of Use
TITLE OF INVENTION: Lepidopteran Insects and Methods of Use
TITLE OF INVENTION: Lepidopteran Insects and Methods of Use
CURRENT APPLICATION NUMBER: US/11/192,967
CURRENT FILING DATE: 2005-07-29
PRIOR PELLING DATE: 2006-11-17
PRIOR APPLICATION NUMBER: 60/166,285
PRIOR APPLICATION NUMBER: 60/166,285
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2.
TOWN THE TERM TOWN TOWN THE TERM TOWN THE TERM TOWN THE TERM TOWN THE TERM TOWN THE TERM THE TERM TOWN THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE TERM THE 
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APPLICANT: Mathis, John P.
APPLICANT: Mathis, John P.
TITLE OF INVENTION: Lepidopteran Insects and Methods of Use
TITLE OF INVENTION: Lepidopteran Insects and Methods of Use
CURRENT APPLICATION NUMBER: US/11/193,715
                                                       7.2%; Score 63; DB 7; Length 325; 22.4%; Pred. No. 15; Atsmatches 44; Indels
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Best Local Similarity 19.7%; Pred. No. 1.6e+02;
Matches 28; Conservative 24; Mismatches 52;
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215 SRAA-----DESIFYMVGBY 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Ostrinia nubilalis
US-11-192-967-2
                                                    Query Match
Best Local Similarity 22.4*
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 ALLGD 137
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   US-11-052-554A-356
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Publication No. US20050288866A1
GENERAL INFORMATION
GENERAL INFORMATION:
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILLE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-06
PRIOR PILING DATE: 2004-07-06
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1. Similarity 27.1%; Pred. No. 30;
36; Conservative 21; Mismatches 53; Indels 23; Gaps
                                                                                                                                                                                                                                         81 TVLLEFYAPWCGHCKQFAPEYEKIANILKD 110
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                                                                                                                                                       Sequence 68, Application US/11196475
Publication No. US20050271682A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Borrelia burgdorferi
US-11-196-475-68
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SOFTWARE: Patentin version 3.3
SEQ ID NO 356
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425 IVKEESKASLADL 437
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Best Local Similarity
Matches 36; Conserva
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Length 1717;

Indels

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TYPE: PRT
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Sequence 8, Application US/11012762

Publication Wo. US20050244815A1

GENERAL INFORMATION:

APPLICANT: Georgia State University Research Foundation, Inc.

TITLE OF INVENTION: Compositions and Methods for Viral Resistance Genes

TILE REFERENCE: GSUI.PCT

CURRENT APPLICATION NUMBER: US/11/012,762

CURRENT FILING DATE: 2004-12-15

PRIOR APPLICATION NUMBER: US (0/390,046

PRIOR APPLICATION NUMBER: US (0/390,046

PRIOR FILING DATE: 2002-06-19

NUMBER OF SEQ ID NOS: 133

SOFTWARE: Patentin Version 3.2

SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 PEDCDFKKD------GLVKRCMGTVTLNQARGSFDISCDKDNKRFALLGDF 138
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26.3%; Pred. No. 69;
tive 11; Mismatches 28; Indels 17;
                                                                                                                                                                                                                                                                                                                     Length 1717;
                                                                                                                                                                                                                                                                                                                 Query Match 7.2%; Score 63; DB 7; Length 171; Best Local Similarity 19.7%; Pred. No. 1.6e+02; Matches 28; Conservative 24; Mismatches 52; Indels
PRIOR APPLICATION NUMBER: 2005-07-29
; PRIOR APPLICATION NUMBER: US/09/715,909
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/166,285
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASESEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1717
; TYPE: non
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Publication No. US20050250678A1
GRWERAL INFORMATION:
APPLICANT: Neose Technologies Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
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; ORGANISM: Ostrinia nubilalis
US-11-193-715-2
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Best Local Similarity 26.31
Matches 20; Conservative
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; ORGANISM: Mus musculus
US-11-012-762-8
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US-11-033-365-198
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69 GDPDTPKPVSFTVKETVCPRTTQQSPEDCDFKKDGLVKRCMGTVTLNQARGSFDISCDKD 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52; Gaps
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APPLICANT: Dorfees, Shawn
APPLICANT: Zopf, David
APPLICANT: Zopf, David
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: O-Linked Glycosylation of peptides
FILE REFERENCE: 040853-01-5138
CURRENT APPLICATION NUMBER: US/11/033,365
CURRENT APPLICATION NUMBER: 00/535,284
PRIOR APPLICATION NUMBER: 60/535,284
PRIOR APPLICATION NUMBER: 60/544,411
PRIOR FILING DATE: 2004-01-08
PRIOR PLILING DATE: 2004-02-20
PRIOR PLILING DATE: 2004-02-20
PRIOR FILING DATE: 2004-02-20
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-05-12
PRIOR FILING DATE: 2004-05-12
NUMBER OF SEQ ID NOS: 213
SOOTWARE: Patentin version 3.2
SOOTWARE: Patentin version 3.2
APPLICANT: Wang, ZhiGuang
APPLICANT: Clausen, Henrik
TILE OF INVENTION O-LINE Glycosylation of peptides
TILE OF INVENTION O-LINE Glycosylation of peptides
CURRENT APPLICATION NUMBER: US/11/033,365
CURRENT APPLICATION NUMBER: 60/535,284
PRIOR PILING DATE: 2005-01-10
PRIOR PILING DATE: 2004-01-08
PRIOR PLING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 60/546,631
PRIOR PLING DATE: 2004-02-20
PRIOR PLING DATE: 2004-03-23
PRIOR PLING DATE: 2004-03-23
PRIOR PLING DATE: 2004-03-24
PRIOR PLING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: 60/555,813
PRIOR PLING DATE: 2004-03-25
PRIOR PLING DATE: 2004-03-25
PRIOR PLING DATE: 2004-03-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.1%; Score 62; DB 7
Best Local Similarity 25.7%; Pred. No. 9.6;
Matches 39; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 G-----IQTLMGRLEDGSPTT----
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Publication No. US20050250678A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 213
SOFTWARE: PatentIn version 3.2
SEQ ID NO 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-033-365-198
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; ORGANISM: Homo sapiens
US-11-033-365-200
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                                                                                    14 SLVLLLLGLVMPLAIIAQVLSYKEAV--LRAI--DGINQRSSDANLYRLL-DLDP--RPT 66
                                             54; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.1%; Score 62; DB 7; Length 301;
Best Local Similarity 21.9%; Pred. No. 18;
Matches 28; Conservative 28; Mismatches 60; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kleenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Russell, William M.
APPLICANT: Altermain, Exic
APPLICANT: Altermain, Exic
APPLICANT: Altermain, Exic
APPLICANT: McAulife, Olivial
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REPERBUCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT APPLICATION NUMBER: 6/551,161
PRIOR PRING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTHARE: PESTSEQ for Windows Version 4.0
SEQ ID NO 362
LENGTH: 301
DB 7; Length 192;
  Query Match 7.1%; Score 62; DB 7; Length 192; Best Local Similarity 25.5%; Pred. No. 9.6; Matches 39; Conservative 23; Mismatches 37; Indels
                                                                                                                                                                                                         126 MGRLEDGSPNTGQ----IFKQTYSKFDTNSHNDDALLKNYGL----
                                                                                                                                                                                                                                                      123 ISCDKDNKRPALLGDPPRKSKEKIGKEFKRIVQ 155
                                                                                                                                                                                                                                                                              Search completed: January 12, 2006, 21:54:25 Job time : 8.52768 secs
                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 362, Application US/11074176; Publication No. US20050250135A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-362
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259 SRKEIERL 266
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US-11-074-176-362
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Published_Applications Mucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_New databases.

Searches run against Mucleic Acid Published_Applications produce two sets of results, with the extensions frapbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions frapbm (Published_Applications_AA_New).

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